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OM protein - protein search, using sw model

Run on: July 27, 2005, 12:32:19 ; Search time 3.12889 Seconds
(without alignments)
381.728 Million cell updates/sec

Title: US-10-030-937-68
Perfect score: 94
Sequence: 1 FSWDNCFEKGKDPVAVIR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	90.4	178	4 US-09-183-841-2	Sequence 2, Appli
2	85	90.4	193	4 US-09-183-841-1	Sequence 1, Appli
3	44	46.8	406	4 US-09-599-360B-98	Sequence 98, Appl
4	44	46.8	1765	4 US-09-270-767-45587	Sequence 45587, A
5	43	45.7	15	4 US-09-069-827A-129	Sequence 129, App
6	43	45.7	590	2 US-08-756-317-12	Sequence 12, Appl
7	43	45.7	619	4 US-09-489-039A-12704	Sequence 12704, A
8	42	44.7	119	4 US-09-270-767-47348	Sequence 47348, A
9	41	43.6	13	4 US-10-158-847-113	Sequence 113, Appl
10	41	43.6	506	2 US-08-635-066-2	Sequence 2, Appli
11	41	43.6	864	4 US-10-101-464A-896	Sequence 896, App
12	41	43.6	956	4 US-09-252-991A-17124	Sequence 17124, A
13	40.5	43.1	246	4 US-09-602-777A-206	Sequence 206, App
14	40.5	43.1	422	4 US-09-602-777A-202	Sequence 202, App
15	40	42.6	19	1 US-08-469-615-18	Sequence 18, Appl
16	40	42.6	19	1 US-08-466-763-18	Sequence 18, Appl
17	40	42.6	19	2 US-08-411-142A-18	Sequence 18, Appl
18	40	42.6	40	1 US-07-901-874B-5	Sequence 5, Appli
19	40	42.6	40	1 US-08-457-865-5	Sequence 5, Appli
20	40	42.6	304	4 US-09-710-279-2190	Sequence 2190, Ap
21	40	42.6	376	4 US-09-270-767-33947	Sequence 33947, A
22	40	42.6	376	4 US-09-270-767-49164	Sequence 49164, A
23	40	42.6	385	2 US-08-516-801-2	Sequence 2, Appli
24	40	42.6	385	3 US-08-248-355-2	Sequence 2, Appli
25	40	42.6	385	4 US-09-167-206-16	Sequence 16, Appl
26	40	42.6	385	5 PCT-US95-06683-2	Sequence 2, Appli
27	40	42.6	399	4 US-09-949-016-10810	Sequence 10810, A

28	40	42.6	415	3 US-09-134-001C-5077	Sequence 5077, Ap
29	40	42.6	488	1 US-07-672-483-1	Sequence 1, Appli
30	40	42.6	490	2 US-08-687-916-24	Sequence 24, Appl
31	40	42.6	490	3 US-09-138-614-24	Sequence 24, Appl
32	40	42.6	619	4 US-09-543-681A-5503	Sequence 5503, Ap
33	40	42.6	621	2 US-08-969-714-1	Sequence 1, Appli
34	40	42.6	645	2 US-08-969-714-3	Sequence 3, Appli
35	39	41.5	13	4 US-10-158-847-105	Sequence 105, App
36	39	41.5	191	4 US-09-489-039A-12833	Sequence 12833, A
37	39	41.5	242	4 US-09-270-767-32046	Sequence 32046, A
38	39	41.5	364	3 US-09-338-671-2	Sequence 2, Appli
39	39	41.5	444	1 US-08-483-140-28	Sequence 28, Appl
40	39	41.5	444	2 US-08-485-938A-32	Sequence 32, Appl
41	39	41.5	658	4 US-09-328-599A-2	Sequence 2, Appli
42	39	41.5	795	3 US-09-031-563-23	Sequence 23, Appl
43	39	41.5	795	4 US-09-392-277-23	Sequence 23, Appl
44	39	41.5	795	4 US-09-258-000-23	Sequence 23, Appl
45	39	41.5	878	4 US-09-556-706B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-183-841-2
; Sequence 2, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanz0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: His tag at residues 1 to 17
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence of GM2 protein using His6 tag
US-09-183-841-2

Query Match 90.4%; Score 85; DB 4; Length 178;
Best Local Similarity 93.8%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSWDNCFEKGKDPVAVIR 16
| | | | | | | | | | | | | | | | | |
Db 19 FSWDNCDEGKDPVAVIR 34

RESULT 2
US-09-183-841-1
; Sequence 1, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanz0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL

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; LOCATION: (33)..(55)
; FEATURE:
; OTHER INFORMATION: residues 56-63 are included in a further precursor
; OTHER INFORMATION: form of the protein
US-09-183-841-1

Query Match      90.4%; Score 85; DB 4; Length 193;
Best Local Similarity 93.8%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FSWDNCFEKGKDPVAVIR 16
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Db      34 FSWDNCDEGKDPVAVIR 49

RESULT 3
US-09-599-360B-98
; Sequence 98, Application US/09599360B
; Patent No. 6548633
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Bougueleret, L.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: GENSET.050CP3
; CURRENT APPLICATION NUMBER: US/09/599,360B
; CURRENT FILING DATE: 2000-06-21
; PRIOR FILING DATE: 1998-12-22
; PRIOR FILING DATE: 1998-12-22
; PRIOR FILING DATE: 1999-06-25
; PRIOR FILING DATE: 1999-06-25
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent.pm
; SEQ ID NO 98
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -35..-1
US-09-599-360B-98

Query Match      46.8%; Score 44; DB 4; Length 406;
Best Local Similarity 46.7%; Pred. No. 35;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1 FSWDNCFEKGKDPAVI 15
      ||||| : ||| :
Db      155 FSWNNITDSLDPATL 169

RESULT 4
US-09-270-767-45587
; Sequence 45587, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45587
; LENGTH: 1765
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: xaa means any amino acid
US-09-270-767-45587
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Query Match      46.8%; Score 44; DB 4; Length 1765;
Best Local Similarity 70.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 WDNCFEKGKDP 12
      | |||||
Db      718 WSGFFEGKDP 727

RESULT 5
US-09-069-827A-129
; Sequence 129, Application US/09069827A
; Patent No. 6617114
; GENERAL INFORMATION:
; APPLICANT: FOWLKES, Dana M
; KAY, Brian K
; FRELINGER, Jeffrey A
; HYDE-DERUYSCHER, Robin P
; TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
; COMPLEMENTARY COMBINATORIAL LIBRARIES
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,827A
; FILING DATE: 30-Apr-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/050,359
; FILING DATE: 31-MAR-1998
; APPLICATION NUMBER: PCT/US97/19638
; FILING DATE: 31-OCT-1997
; APPLICATION NUMBER: US 08/740,671
; FILING DATE: 31-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOWLKES=4C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 129:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 129:
US-09-069-827A-129

Query Match      45.7%; Score 43; DB 4; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.5;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 FSWDNCFEKG 10
      | ||| :
Db      6 FFWDGCFESR 15

RESULT 6
US-08-756-317-12
; Sequence 12, Application US/08756317
```

Patent No. 5849894
 GENERAL INFORMATION:
 APPLICANT: Clemente, Thomas E.
 APPLICANT: Kishore, Ganesh M.
 APPLICANT: Mitsky, Timothy A.
 APPLICANT: Stark, David M.
 TITLE OF INVENTION: Improved Rhodospirillum Rubrum
 TITLE OF INVENTION: Poly-B-Hydroxyalkanoate Synthase
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: TX
 COUNTRY: USA
 ZIP: 77210-4433
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/756,317
 FILING DATE: 25-NOV-1996
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/007,693
 FILING DATE: 29-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Patterson, Melinda L.
 REGISTRATION NUMBER: 33,062
 REFERENCE/DOCKET NUMBER: MOBT:008
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (713) 787-1400
 TELEFAX: (713) 787-1440
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 590 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-756-317-12

Query Match 45.7%; Score 43; DB 2; Length 590;
 Best Local Similarity 66.7%; Pred. No. 75;
 Matches 6; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

Qy 3 WDNCFEGKD 11
 |||||
 Db 486 WDTFCRGAD 494

RESULT 7
 US-09-489-039A-12704
 Sequence 12704, Application US/09489039A
 Patent No. 6610836
 GENERAL INFORMATION:
 APPLICANT: Gary Breton et. al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709.2004001
 CURRENT APPLICATION NUMBER: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 12704
 LENGTH: 619
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-12704

Query Match 45.7%; Score 43; DB 4; Length 619;

Best Local Similarity 50.0%; Pred. No. 79;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 3 WDNCFEGKDPVAVIR 16
 |:|:|:|:|
 Db 478 WNNTRSGEDPVAIR 491

RESULT 8
 US-09-270-767-47348
 Sequence 47348, Application US/09270767
 Patent No. 6703491
 GENERAL INFORMATION:
 APPLICANT: Homburger et al.
 TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 FILE REFERENCE: File Reference: 7326-094
 CURRENT APPLICATION NUMBER: US/09/270,767
 CURRENT FILING DATE: 1999-03-17
 NUMBER OF SEQ ID NOS: 62517
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 47348
 LENGTH: 119
 TYPE: PRT
 ORGANISM: Drosophila melanogaster
 US-09-270-767-47348

Query Match 44.7%; Score 42; DB 4; Length 119;
 Best Local Similarity 50.0%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 WDNCFEGKDPVAV 14
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 Db 97 WRECFEGFQPTI 108

RESULT 9
 US-10-158-847-113
 Sequence 113, Application US/10158847
 Patent No. 6592865
 GENERAL INFORMATION:
 APPLICANT: Tom Parry et al.
 TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
 FILE REFERENCE: PF557
 CURRENT APPLICATION NUMBER: US/10/158,847
 CURRENT FILING DATE: 2002-06-03
 PRIOR APPLICATION NUMBER: 60/295,004
 PRIOR FILING DATE: 2001-06-04
 NUMBER OF SEQ ID NOS: 158
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 113
 LENGTH: 13
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-158-847-113

Query Match 43.6%; Score 41; DB 4; Length 13;
 Best Local Similarity 66.7%; Pred. No. 2.7;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FSWDNCPEG 9
 |||||
 Db 5 FDWDECFGLG 13

RESULT 10
 US-08-635-066-2
 Sequence 2, Application US/08635066
 Patent No. 5945580
 GENERAL INFORMATION:
 APPLICANT: Dunsmuir, Pamela
 APPLICANT: Harpster, Mark H.
 TITLE OF INVENTION: Capsicum Hemicellulase Polynucleotides
 TITLE OF INVENTION: and Polypeptides

; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,066
; FILING DATE: 19-APR-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 012176-005500
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 506 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-635-066-2

Query Match 43.6%; Score 41; DB 2; Length 506;
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FSWDNCFEG 9
Db 266 FSWDNKFAG 274

RESULT 11
US-10-101-464A-896
; Sequence 896, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020C2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 896
; LENGTH: 864
; TYPE: PRT
; ORGANISM: Pinus radiata
; US-10-101-464A-896

Query Match 43.6%; Score 41; DB 4; Length 864;
Best Local Similarity 58.3%; Pred. No. 2.4e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 NCFEGKDPVIR 16
Db 402 NCFSGAIPSLIR 413

RESULT 12
US-09-252-991A-17124
; Sequence 17124, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17124
; LENGTH: 956
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-17124

Query Match 43.6%; Score 41; DB 4; Length 956;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 DNCFEGKDP 12
Db 291 EHCFEHGDP 299

RESULT 13
US-09-602-777A-206
; Sequence 206, Application US/09602777A
; Patent No. 6831165
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128CP
; CURRENT APPLICATION NUMBER: US/09/602,777A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932924.9


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; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932928.1
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932930.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932933.8
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932935.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932973.7
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933002.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933003.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941390.8
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941391.6
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 206
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-602-777A-206

Query Match      43.1%; Score 40.5; DB 4; Length 246;
Best Local Similarity 34.6%; Pred. No. 75;
Matches 9; Conservative 1; Mismatches 5; Indels 11; Gaps 1;

Qy      1 FSWDNCF-----EGKDPAVI 15
      |||||
Db      151 FSWKNCLSESGSHLPVHDGSDAVI 176

RESULT 14
US-09-602-777A-202
; Sequence 202, Application US/09602777A
; Patent No. 6831165
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128CP
; CURRENT APPLICATION NUMBER: US/09/602,777A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
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; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932924.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932928.1
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932930.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932933.8
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932935.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932973.7
; PRIOR APPLICATION NUMBER: DE 19933002.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933003.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941390.8
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941391.6
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 202
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-602-777A-202

Query Match      43.1%; Score 40.5; DB 4; Length 422;
Best Local Similarity 34.6%; Pred. No. 1.3e+02;
Matches 9; Conservative 1; Mismatches 5; Indels 11; Gaps 1;

Qy      1 FSWDNCF-----EGKDPAVI 15
      |||||
Db      145 FSWKNCLSESGSHLPVHDGSDAVI 170

RESULT 15
US-08-469-615-18
; Sequence 18, Application US/08469615
; Patent No. 5622703
; GENERAL INFORMATION:
; APPLICANT: Berzofsky, Jay A.
; APPLICANT: Kurata, Akihiko
; TITLE OF INVENTION: Immunodominant Sites of HTLV-I Envelope
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,615
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,118
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30330
REFERENCE/DOCKET NUMBER: 1173-500P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: htlv-I
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..19
OTHER INFORMATION: /label= peptid_vle9
US-08-469-615-18

Query Match 42.6%; Score 40; DB 1; Length 19;
Best Local Similarity 33.3%; Pred. No. 6;
Matches 5; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 FSWDNCFEGKDPRAVI 15
|:|:|:|:|:
Db 4 FNTWTHCFDPQIQIAIV 18

Search completed: July 27, 2005, 18:59:20
Job time : 5.12889 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 18:09:01 ; Search time 35.0578 Seconds
(without alignments)
177.532 Million cell updates/sec

Title: US-10-030-937-68

Perfect score: 94

Sequence: 1 FSWDNCFEGKDPVIR 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	90.4	193	15	US-10-170-385-389
2	85	90.4	193	16	US-10-723-860-529
3	57	60.6	126	10	US-09-764-891-4977
4	57	60.6	191	15	US-10-264-049-2611
5	47	50.0	620	15	US-10-369-493-14781
6	47	50.0	623	15	US-10-369-493-14935
7	47	50.0	649	15	US-10-369-493-11373
8	46	48.9	101	16	US-10-425-115-246626
9	46	48.9	211	15	US-10-225-066A-96
10	46	48.9	211	15	US-10-374-780A-2846
11	46	48.9	211	17	US-10-732-923-5447
					Sequence 389, App
					Sequence 529, App
					Sequence 4977, Ap
					Sequence 2611, Ap
					Sequence 14781, A
					Sequence 14935, A
					Sequence 11373, A
					Sequence 246626,
					Sequence 96, Appl
					Sequence 2846, Ap
					Sequence 5447, Ap

12	46	48.9	588	15	US-10-282-122A-77389	Sequence 77389, A
13	45	47.9	493	15	US-10-369-493-4327	Sequence 4327, Ap
14	45	47.9	493	15	US-10-369-493-7083	Sequence 7083, Ap
15	45	47.9	1411	15	US-10-282-122A-43060	Sequence 43060, A
16	44	46.8	74	16	US-10-437-963-110611	Sequence 110611,
17	44	46.8	90	16	US-10-425-115-350643	Sequence 350643,
18	44	46.8	108	16	US-10-425-115-351913	Sequence 351913,
19	44	46.8	131	17	US-10-935-098-99	Sequence 99, Appl
20	44	46.8	132	9	US-09-739-907-99	Sequence 99, Appl
21	44	46.8	132	11	US-09-938-671-99	Sequence 87, Appl
22	44	46.8	172	9	US-09-739-907-87	Sequence 87, Appl
23	44	46.8	172	11	US-09-938-671-87	Sequence 87, Appl
24	44	46.8	172	17	US-10-935-098-87	Sequence 87, Appl
25	44	46.8	177	11	US-09-833-245-1188	Sequence 1188, Ap
26	44	46.8	182	9	US-09-739-907-191	Sequence 191, App
27	44	46.8	182	11	US-09-938-671-191	Sequence 191, App
28	44	46.8	182	17	US-10-935-098-191	Sequence 191, App
29	44	46.8	213	16	US-10-425-115-224812	Sequence 224812,
30	44	46.8	330	11	US-09-833-245-1189	Sequence 1189, Ap
31	44	46.8	357	17	US-10-495-148-44	Sequence 44, Appl
32	44	46.8	406	9	US-09-731-872-245	Sequence 245, App
33	44	46.8	406	10	US-09-876-997-245	Sequence 245, App
34	44	46.8	406	11	US-09-978-360A-430	Sequence 430, App
35	44	46.8	406	14	US-10-028-072-66	Sequence 66, Appl
36	44	46.8	406	14	US-10-028-072-258	Sequence 258, App
37	44	46.8	406	14	US-10-140-808-66	Sequence 66, Appl
38	44	46.8	406	14	US-10-140-808-258	Sequence 258, App
39	44	46.8	406	14	US-10-121-049-66	Sequence 66, Appl
40	44	46.8	406	14	US-10-121-049-258	Sequence 258, App
41	44	46.8	406	14	US-10-123-904-66	Sequence 66, Appl
42	44	46.8	406	14	US-10-123-904-258	Sequence 258, App
43	44	46.8	406	14	US-10-140-470-66	Sequence 66, Appl
44	44	46.8	406	14	US-10-140-470-258	Sequence 258, App
45	44	46.8	406	14	US-10-175-746-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1

US-10-170-385-389
; Sequence 389, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-389

Query Match 90.4%; Score 85; DB 15; Length 193;
Best Local Similarity 93.8%; Pred.No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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; NAME/KEY: unsure
; LOCATION: (1)..(620)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-14781

Query Match          50.0%; Score 47; DB 15; Length 620;
Best Local Similarity 56.2%; Pred. No. 40;
Matches 9; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY      2 SWDNCPEG--KDP AVI 15
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Db      459 SWNGFEGLTDDPAIV 474

RESULT 6
US-10-369-493-14935
; Sequence 14935, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14935
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(623)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-14935

Query Match          50.0%; Score 47; DB 15; Length 623;
Best Local Similarity 56.2%; Pred. No. 41;
Matches 9; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY      2 SWDNCPEG--KDP AVI 15
      ||:||||| |||::
Db      458 SWNGFEGLTDDPAIV 473

RESULT 7
US-10-369-493-11373
; Sequence 11373, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 11373
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
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US-10-369-493-11373

Query Match          50.0%; Score 47; DB 15; Length 649;
Best Local Similarity 56.2%; Pred. No. 42;
Matches 9; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY      2 SWDNCPEG--KDP AVI 15
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Db      465 SWNGFEGLTDDPAIV 480

RESULT 8
US-10-425-115-246626
; Sequence 246626, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 246626
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_156506C.1.pep
US-10-425-115-246626

Query Match          48.9%; Score 46; DB 16; Length 101;
Best Local Similarity 46.2%; Pred. No. 8.8;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      3 WDNCFEGKDP AVI 15
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Db      28 WNSCFHGPEPPVM 40

RESULT 9
US-10-225-066A-96
; Sequence 96, Application US/10225066A
; Publication No. US20030226173A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: ADAM, Luc J
; APPLICANT: DUBELL, Arnold T
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: PILGRIM, Marsha L
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: REUBER, T. Lynne
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omaira
; APPLICANT: YU, Guo-Liang
; APPLICANT: BROUN, Pierre E
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MBI0036-2 US
; CURRENT APPLICATION NUMBER: US/10/225,066A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/837,444
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
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; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 1122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-96

Query Match      48.9%; Score 46; DB 15; Length 211;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 SWDNCFEKGD 11
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Db      169 SWYNCFDGDD 178

RESULT 10
US-10-374-780A-2846
; Sequence 2846, Application US/10374780A
; Publication No. US20040019927A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddle, James
; APPLICANT: Broun, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2846
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G2294
US-10-374-780A-2846

Query Match      48.9%; Score 46; DB 15; Length 211;
Best Local Similarity 70.0%; Pred. No. 19;

PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 1122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 96
LENGTH: 211
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-225-066A-96

Query Match      48.9%; Score 46; DB 17; Length 211;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 SWDNCFEKGD 11
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Db      169 SWYNCFDGDD 178

RESULT 11
US-10-732-923-5447
; Sequence 5447, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 5447
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-732-923-5447

Query Match      48.9%; Score 46; DB 17; Length 211;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 SWDNCFEKGD 11
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Db      169 SWYNCFDGDD 178

RESULT 12
US-10-282-122A-77389
; Sequence 77389, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
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; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77389
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-282-122A-77389

Query Match      48.9%; Score 46; DB 15; Length 588;
Best Local Similarity 57.1%; Pred. No. 56;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      3 WDNCFEGKDPVIR 16
      |||: |||
Db      447 WENSKGEDPVIR 460

RESULT 13
US-10-369-493-4327
; Sequence 4327, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4327
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-369-493-4327

Query Match      47.9%; Score 45; DB 15; Length 493;
Best Local Similarity 58.3%; Pred. No. 69;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 WDNCFEGKDPVIR 14
      |||: |||
Db      449 WVNCYQVMDPAV 460

RESULT 14
US-10-369-493-7083
; Sequence 7083, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 7083
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; LENGTH: 493
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
US-10-369-493-7083

Query Match      47.9%; Score 45; DB 15; Length 493;
Best Local Similarity 58.3%; Pred. No. 69;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 WDNCFEGKDPVIR 14
      |||: |||
Db      449 WVNCYQVMDPAV 460

RESULT 15
US-10-282-122A-43060
; Sequence 43060, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43060
; LENGTH: 1411
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-282-122A-43060

Query Match      47.9%; Score 45; DB 15; Length 1411;
Best Local Similarity 42.9%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      3 WDNCFEGKDPVIR 16
      |||: |||
Db      1354 WDEIFSGKDEKIVK 1367
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Search completed: July 27, 2005, 19:16:51
Job time : 36.0578 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 18:58:36 ; Search time 3.05778 Seconds
(without alignments)
390.606 Million cell updates/sec

Title: US-10-030-937-68
Perfect score: 16
Sequence: 1 FSWDNCFEGKDPVIR 16

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Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	56.2	178	4	US-09-183-841-2
2	9	56.2	193	4	US-09-183-841-1
3	6	37.5	127	4	US-09-252-991A-18412
4	6	37.5	185	4	US-09-248-796A-16879
5	6	37.5	243	4	US-09-541-759-7
6	6	37.5	257	4	US-09-949-016-7490
7	6	37.5	297	1	US-08-534-910B-6
8	6	37.5	297	1	US-08-534-910B-7
9	6	37.5	297	1	US-08-534-910B-8
10	6	37.5	297	1	US-08-534-910B-9
11	6	37.5	297	1	US-08-534-910B-10
12	6	37.5	297	3	US-08-886-466-2
13	6	37.5	297	3	US-09-475-304-2
14	6	37.5	297	3	US-09-101-126-3
15	6	37.5	297	3	US-09-367-528A-1
16	6	37.5	297	3	US-09-367-528A-3
17	6	37.5	297	3	US-09-367-528A-5
18	6	37.5	1765	4	US-09-270-767-45587
19	5	31.2	25	1	US-07-706-699-1
20	5	31.2	25	1	US-07-998-931-1
21	5	31.2	25	4	US-09-042-460-52
22	5	31.2	30	3	US-08-851-843A-155
23	5	31.2	30	3	US-08-974-549A-275
24	5	31.2	30	3	US-08-854-050-155
25	5	31.2	30	3	US-09-430-323-155
26	5	31.2	30	4	US-09-402-181B-275
27	5	31.2	30	4	US-09-721-456-275

28	5	31.2	30	4	US-09-766-253-155	Sequence 155, App
29	5	31.2	35	2	US-08-737-716-12	Sequence 12, Appl
30	5	31.2	54	3	US-08-974-549A-25	Sequence 25, Appl
31	5	31.2	54	4	US-08-912-951-25	Sequence 25, Appl
32	5	31.2	54	4	US-09-402-181B-25	Sequence 25, Appl
33	5	31.2	54	4	US-09-721-456-25	Sequence 25, Appl
34	5	31.2	64	4	US-09-205-258-774	Sequence 774, App
35	5	31.2	73	4	US-09-438-185A-1008	Sequence 1008, Ap
36	5	31.2	78	4	US-09-489-039A-11104	Sequence 11104, A
37	5	31.2	82	4	US-09-198-452A-1142	Sequence 1142, Ap
38	5	31.2	82	4	US-09-270-767-58568	Sequence 58568, A
39	5	31.2	82	4	US-09-513-999C-5870	Sequence 5870, Ap
40	5	31.2	107	4	US-09-489-039A-11962	Sequence 11962, A
41	5	31.2	127	4	US-09-270-767-47503	Sequence 47503, A
42	5	31.2	145	4	US-09-270-767-43226	Sequence 43226, A
43	5	31.2	149	4	US-09-270-767-40911	Sequence 40911, A
44	5	31.2	149	4	US-09-270-767-56127	Sequence 56127, A
45	5	31.2	158	4	US-09-107-433-3844	Sequence 3844, Ap

ALIGNMENTS

RESULT 1
US-09-183-841-2
; Sequence 2, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanz0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: His tag at residues 1 to 17
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence of GM2 protein using His6 tag
US-09-183-841-2

Query Match 56.2%; Score 9; DB 4; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGKDPVIR 16
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Db 26 EGKDPVIR 34

RESULT 2
US-09-183-841-1
; Sequence 1, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanz0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL

; LOCATION: (33)..(55)
 ; FEATURE:
 ; OTHER INFORMATION: residues 56-63 are included in a further precursor
 ; OTHER INFORMATION: form of the protein
 US-09-183-841-1

Query Match 56.2%; Score 9; DB 4; Length 193;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGKDPVIR 16
 |||||
 Db 41 EGKDPVIR 49

RESULT 3

US-09-252-991A-18412
 ; Sequence 18412, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 18412
 ; LENGTH: 127
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-18412

Query Match 37.5%; Score 6; DB 4; Length 127;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGKDPV 13
 |||||
 Db 4 EGKDPV 9

RESULT 4

US-09-248-796A-16879
 ; Sequence 16879, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 16879
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 US-09-248-796A-16879

Query Match 37.5%; Score 6; DB 4; Length 185;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KDPVIR 15

Db 171 KDPVIR 176
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RESULT 5

US-09-541-759-7
 ; Sequence 7, Application US/09541759
 ; Patent No. 6723322
 ; GENERAL INFORMATION:
 ; APPLICANT: Lustigman, Sara
 ; APPLICANT: Pearlman, Eric
 ; APPLICANT: Unnasch, Thomas
 ; TITLE OF INVENTION: ANGIOGENIC ONCHOCERCA VOLVULUS PROTEINS AND USES THEREOF
 ; FILE REFERENCE: 63475/252
 ; CURRENT APPLICATION NUMBER: US/09/541,759
 ; CURRENT FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 7
 ; LENGTH: 243
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-541-759-7

Query Match 37.5%; Score 6; DB 4; Length 243;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGKDPV 13
 |||||
 Db 20 EGKDPV 25

RESULT 6

US-09-949-016-7490
 ; Sequence 7490, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7490
 ; LENGTH: 257
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-7490

Query Match 37.5%; Score 6; DB 4; Length 257;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGKDPV 13
 |||||
 Db 34 EGKDPV 39

RESULT 7

US-08-534-910B-6
 ; Sequence 6, Application US/08534910B
 ; Patent No. 5766911
 ; GENERAL INFORMATION:
 ; APPLICANT: KOIKE, Ayumi


```

; APPLICATION NUMBER: JP 7-25253
; FILING DATE: 14-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Toffenetti, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 77670/398
; TELEPHONE: (202)429-1776
; TELEFAX: (202)429-0796
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Bacillus stearothermophilus
;
US-08-534-910B-8
;
Query Match 37.5%; Score 6; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GKDPV 14
Db 62 GKDPV 67

RESULT 10
US-08-534-910B-9
; Sequence 9, Application US/08534910B
; Patent No. 5766911
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Ayumi
; APPLICANT: OBATA, Shusei
; APPLICANT: NISHINO, Tokuzo
; APPLICANT: OHNUMA, Shinichi
; APPLICANT: NAKAZAWA, Takeshi
; APPLICANT: OGURA, Kyoza
; APPLICANT: KOYAMA, Tanetoshi
; TITLE OF INVENTION: Mutated Farnesylldiphosphate Synthase Capable
; TITLE OF INVENTION: Of Synthesizing Geranylgeranyldiphosphate And Gene Coding Ther
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.25" Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
; SOFTWARE: IBM/Word Perfect 6.1 Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/534,910B
; FILING DATE: 28-SEPT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-25253
; FILING DATE: 14-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Toffenetti, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 77670/398
; TELEPHONE: (202)429-1776
; TELEFAX: (202)429-0796
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Bacillus stearothermophilus
;
US-08-534-910B-9
;
Query Match 37.5%; Score 6; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GKDPV 14
Db 62 GKDPV 67

RESULT 11
US-08-534-910B-10
; Sequence 10, Application US/08534910B
; Patent No. 5766911
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Ayumi
; APPLICANT: OBATA, Shusei
; APPLICANT: NISHINO, Tokuzo
; APPLICANT: OHNUMA, Shinichi
; APPLICANT: NAKAZAWA, Takeshi
; APPLICANT: OGURA, Kyoza
; APPLICANT: KOYAMA, Tanetoshi
; TITLE OF INVENTION: Mutated Farnesylldiphosphate Synthase Capable
; TITLE OF INVENTION: Of Synthesizing Geranylgeranyldiphosphate And Gene Coding Ther
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.25" Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
; SOFTWARE: IBM/Word Perfect 6.1 Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/534,910B
; FILING DATE: 28-SEPT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-25253
; FILING DATE: 14-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Toffenetti, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 77670/398
; TELEPHONE: (202)429-1776
; TELEFAX: (202)429-0796
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Bacillus stearothermophilus
;
US-08-534-910B-10
;
Query Match 37.5%; Score 6; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GKDPV 14
Db 62 GKDPV 67
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Bacillus stearothermophilus
;
US-08-534-910B-9
;
Query Match 37.5%; Score 6; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GKDPV 14
Db 62 GKDPV 67

RESULT 11
US-08-534-910B-10
; Sequence 10, Application US/08534910B
; Patent No. 5766911
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Ayumi
; APPLICANT: OBATA, Shusei
; APPLICANT: NISHINO, Tokuzo
; APPLICANT: OHNUMA, Shinichi
; APPLICANT: NAKAZAWA, Takeshi
; APPLICANT: OGURA, Kyoza
; APPLICANT: KOYAMA, Tanetoshi
; TITLE OF INVENTION: Mutated Farnesylldiphosphate Synthase Capable
; TITLE OF INVENTION: Of Synthesizing Geranylgeranyldiphosphate And Gene Coding Ther
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.25" Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
; SOFTWARE: IBM/Word Perfect 6.1 Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/534,910B
; FILING DATE: 28-SEPT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-25253
; FILING DATE: 14-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Toffenetti, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 77670/398
; TELEPHONE: (202)429-1776
; TELEFAX: (202)429-0796
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Bacillus stearothermophilus
;
US-08-534-910B-10
;
Query Match 37.5%; Score 6; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GKDPV 14
Db 62 GKDPV 67
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RESULT 12

US-08-886-466-2
; Sequence 2, Application US/08886466C
; Patent No. 6040165

; GENERAL INFORMATION:

; APPLICANT: Narita, Keishi
; APPLICANT: Ishida, Chika
; APPLICANT: Takeuchi, Yoshie
; APPLICANT: Ohto, Chikara
; APPLICANT: Ohnuma, Shinichi
; APPLICANT: Nishino, Tokuzo
; TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE

; FILE REFERENCE: 77670/494

; CURRENT APPLICATION NUMBER: US/08/886,466C

; CURRENT FILING DATE: 1997-07-10

; EARLIER APPLICATION NUMBER: JP 8-191635

; EARLIER FILING DATE: 1996-07-03

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 297

; TYPE: PRT

; ORGANISM: Bacillus stearothermophilus

US-08-886-466-2

Query Match

37.5%; Score 6; DB 3; Length 297;

Best Local Similarity 100.0%; Pred. No. 29;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GKDPV 14

Db 62 GKDPV 67

RESULT 13

US-09-475-304-2

; Sequence 2, Application US/09475304

; Patent No. 6225096

; GENERAL INFORMATION:

; APPLICANT: Narita, Keishi

; APPLICANT: Ishida, Chika

; APPLICANT: Takeuchi, Yoshie

; APPLICANT: Ohto, Chikara

; APPLICANT: Ohnuma, Shinichi

; APPLICANT: Nishino, Tokuzo

; TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE

; FILE REFERENCE: 77670/494

; CURRENT APPLICATION NUMBER: US/09/475,304

; CURRENT FILING DATE: 1999-12-30

; EARLIER APPLICATION NUMBER: JP 8-191635

; EARLIER FILING DATE: 1996-07-03

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 297

; TYPE: PRT

; ORGANISM: Bacillus stearothermophilus

US-09-475-304-2

Query Match

37.5%; Score 6; DB 3; Length 297;

Best Local Similarity 100.0%; Pred. No. 29;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GKDPV 14

Db 62 GKDPV 67

RESULT 14

US-09-101-126-3

; Sequence 3, Application US/09101126

; Patent No. 6316216

; GENERAL INFORMATION:

; APPLICANT: OHTO, CHIKARA

; APPLICANT: NAKANE, HIROYUKI

; APPLICANT: NISHINO, TOKUZO

; APPLICANT: OHNUMA, SHINICHI

; APPLICANT: HIROOKA, KAZUTAKE

; TITLE OF INVENTION: MUTATED PRENYL DIPHOSPHATE SYNTHASES

; FILE REFERENCE: 77670/566

; CURRENT APPLICATION NUMBER: US/09/101,126

; CURRENT FILING DATE: 1999-04-27

; EARLIER APPLICATION NUMBER: PCT/JP97/03921

; EARLIER FILING DATE: 1997-10-29

; EARLIER APPLICATION NUMBER: JP 8-307506

; EARLIER FILING DATE: 1996-11-05

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 297

; TYPE: PRT

; ORGANISM: Bacillus stearothermophilus

; FEATURE:

; OTHER INFORMATION: 86-92 is an Asp-rich domain

US-09-101-126-3

Query Match

37.5%; Score 6; DB 3; Length 297;

Best Local Similarity 100.0%; Pred. No. 29;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GKDPV 14

Db 62 GKDPV 67

RESULT 15

US-09-367-528A-1

; Sequence 1, Application US/09367528A

; Patent No. 6395525

; GENERAL INFORMATION:

; APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA

; TITLE OF INVENTION: Geranyl Diphosphate Synthetase Gene

; FILE REFERENCE: PH-586

; CURRENT APPLICATION NUMBER: US/09/367,528A

; CURRENT FILING DATE: 1999-08-16

; PRIOR APPLICATION NUMBER: JP97/346686

; PRIOR FILING DATE: 1997-12-16

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 297

; TYPE: PRT

; ORGANISM: Bacillus stearothermophilus

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: 82

; OTHER INFORMATION: Xaa represents Val, Leu, Ile, Thr, Asp, Glu, Asn, Gln, Lys,

; OTHER INFORMATION: Arg, Cys, Met, Phe, Tyr, Trp, His or Pro.

US-09-367-528A-1

Query Match

37.5%; Score 6; DB 3; Length 297;

Best Local Similarity 100.0%; Pred. No. 29;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GKDPV 14

Db 62 GKDPV 67

Search completed: July 27, 2005, 19:17:42

Job time : 4.05778 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 19:08:40 ; Search time 8.8889 Seconds
(without alignments)
700.186 Million cell updates/sec

Title: US-10-030-937-68

Perfect score: 16

Sequence: 1 FSWDNCFEKDPVIR 16

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1741741 seqs, 388992284 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
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- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	9	56.2	193	15	US-10-170-385-389
2	9	56.2	193	16	US-10-723-860-529
3	6	37.5	85	11	US-09-864-408A-5064
4	6	37.5	105	15	US-10-424-599-274901
5	6	37.5	126	9	US-09-815-242-5124
6	6	37.5	126	15	US-10-282-122A-43427
7	6	37.5	143	10	US-09-764-891-4060
8	6	37.5	160	15	US-10-424-599-260239
9	6	37.5	199	15	US-10-383-201-8
10	6	37.5	203	15	US-10-383-201-6
11	6	37.5	217	15	US-10-383-201-4

12	6	37.5	243	15	US-10-383-201-2	Sequence 2, Appli
13	6	37.5	297	9	US-09-367-528A-1	Sequence 1, Appli
14	6	37.5	297	9	US-09-367-528A-3	Sequence 3, Appli
15	6	37.5	297	9	US-09-367-528A-5	Sequence 5, Appli
16	6	37.5	297	15	US-10-462-698A-76	Sequence 76, Appli
17	6	37.5	308	15	US-10-282-122A-52133	Sequence 52133, A
18	6	37.5	329	15	US-10-369-493-588	Sequence 588, App
19	6	37.5	329	17	US-10-732-923-5280	Sequence 5280, Ap
20	6	37.5	379	15	US-10-282-122A-60813	Sequence 60813, A
21	6	37.5	391	16	US-10-437-963-200217	Sequence 200217,
22	6	37.5	403	15	US-10-369-493-20145	Sequence 20145, A
23	6	37.5	423	18	US-10-637-831-6	Sequence 6, Appli
24	6	37.5	434	14	US-10-171-404A-46	Sequence 46, Appli
25	6	37.5	434	18	US-10-637-831-4	Sequence 4, Appli
26	6	37.5	446	15	US-10-282-122A-49297	Sequence 49297, A
27	6	37.5	471	16	US-10-437-963-203808	Sequence 203808,
28	6	37.5	474	17	US-10-732-923-1109	Sequence 1109, Ap
29	6	37.5	523	16	US-10-672-282-10	Sequence 10, Appli
30	6	37.5	526	16	US-10-672-282-3	Sequence 3, Appli
31	6	37.5	526	16	US-10-739-930-6665	Sequence 6665, Ap
32	6	37.5	641	16	US-10-437-963-137331	Sequence 137331,
33	6	37.5	757	16	US-10-437-963-185490	Sequence 185490,
34	6	37.5	825	16	US-10-408-765A-2285	Sequence 2285, Ap
35	6	37.5	912	16	US-10-623-813-7	Sequence 7, Appli
36	6	37.5	958	16	US-10-437-963-137333	Sequence 137333,
37	6	37.5	1036	16	US-10-437-963-126411	Sequence 126411,
38	6	37.5	1179	16	US-10-437-963-137323	Sequence 137323,
39	6	37.5	1191	16	US-10-437-963-126407	Sequence 126407,
40	6	37.5	1741	16	US-10-437-963-126375	Sequence 126375,
41	6	37.5	2112	16	US-10-437-963-126488	Sequence 126488,
42	6	37.5	3250	15	US-10-369-493-20151	Sequence 20151, A
43	5	31.2	13	15	US-10-468-370-631	Sequence 631, App
44	5	31.2	13	15	US-10-468-370-632	Sequence 632, App
45	5	31.2	13	15	US-10-468-370-633	Sequence 633, App

ALIGNMENTS

RESULT 1
US-10-170-385-389
; Sequence 389, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-389

Query Match 56.2%; Score 9; DB 15; Length 193;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGKDPVAVIR 16
| | | | | | | |
Db 41 EGKDPVAVIR 49

RESULT 2

US-10-723-860-529
; Sequence 529, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 529
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-529

Query Match 56.2%; Score 9; DB 16; Length 193;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGKDPVAVIR 16
| | | | | | | |
Db 41 EGKDPVAVIR 49

RESULT 3

US-09-864-408A-5064
; Sequence 5064, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Encod
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5064
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
US-09-864-408A-5064

Query Match 37.5%; Score 6; DB 11; Length 85;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 DPAVIR 16
| | | | | | | |
Db 73 DPAVIR 78

RESULT 4

US-10-424-599-274901
; Sequence 274901, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 274901
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(105)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_90256C.1.pep
US-10-424-599-274901

Query Match 37.5%; Score 6; DB 15; Length 105;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGKDPA 13
| | | | | | | |
Db 42 EGKDPA 47

RESULT 5

US-09-815-242-5124
; Sequence 5124, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5124
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-815-242-5124

Query Match 37.5%; Score 6; DB 9; Length 126;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGKDP A 13
Db 3 EGKDP A 8

RESULT 6

US-10-282-122A-43427
; Sequence 43427, Application US/10282122A
; Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 43427

LENGTH: 126

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-10-282-122A-43427

Query Match 37.5%; Score 6; DB 15; Length 126;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGKDP A 13
Db 3 EGKDP A 8

RESULT 7

US-09-764-891-4060

; Sequence 4060, Application US/09764891

Publication No. US20030077808A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC006

CURRENT APPLICATION NUMBER: US/09/764,891

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 10231

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4060

LENGTH: 143

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (65)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (126)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (131)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-764-891-4060

Query Match 37.5%; Score 6; DB 10; Length 143;

Best Local Similarity 100.0%; Pred. No. 76;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGKDP A 13

Db 76 EGKDP A 81

RESULT 8

US-10-424-599-260239

; Sequence 260239, Application US/10424599

; Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 260239

LENGTH: 160

TYPE: PRT

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_77019C.1.pep

US-10-424-599-260239

Query Match 37.5%; Score 6; DB 15; Length 160;

Best Local Similarity 100.0%; Pred. No. 84;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 DPAVIR 16

Db 99 DPAVIR 104

RESULT 9

US-10-383-201-8

; Sequence 8, Application US/10383201

; Publication No. US20040029226A1

GENERAL INFORMATION:

APPLICANT: Alsobrook II, John et al.

```
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-568A
; CURRENT APPLICATION NUMBER: US/10/383,201
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 10/029020
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/365,984
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/372,022
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/389,143
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/391,779
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/410,755
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 60/412,957
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 10/051,874
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/366,928
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 8
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-383-201-8

Query Match      37.5%; Score 6; DB 15; Length 199;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 EGKDPA 13
      |||||
Db      2 EGKDPA 7

RESULT 10
US-10-383-201-6
; Sequence 6, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-568A
; CURRENT APPLICATION NUMBER: US/10/383,201
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 10/029020
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/365,984
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/372,022
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/389,143
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/391,779
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/410,755
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 60/412,957
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 10/051,874
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/366,928
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-383-201-4

Query Match      37.5%; Score 6; DB 15; Length 217;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 EGKDPA 13
      |||||
Db      20 EGKDPA 25

RESULT 12
US-10-383-201-2
; Sequence 2, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-568A
; CURRENT APPLICATION NUMBER: US/10/383,201
; CURRENT FILING DATE: 2003-03-06
; SOFTWARE: CuraSeqList version 0.1
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; SEQ ID NO 6
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-383-201-6

Query Match      37.5%; Score 6; DB 15; Length 203;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 EGKDPA 13
      |||||
Db      4 EGKDPA 9

RESULT 11
US-10-383-201-4
; Sequence 4, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-568A
; CURRENT APPLICATION NUMBER: US/10/383,201
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 10/029020
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/365,984
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/372,022
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/389,143
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/391,779
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/410,755
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 60/412,957
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 10/051,874
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/366,928
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-383-201-4

Query Match      37.5%; Score 6; DB 15; Length 217;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 EGKDPA 13
      |||||
Db      20 EGKDPA 25

RESULT 12
US-10-383-201-2
; Sequence 2, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-568A
; CURRENT APPLICATION NUMBER: US/10/383,201
; CURRENT FILING DATE: 2003-03-06
; SOFTWARE: CuraSeqList version 0.1
```



```

; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/365,984
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/372,022
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/389,143
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/391,779
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/410,755
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 60/412,957
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 10/051,874
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/366,928
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 2
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-383-201-2

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Query Match      37.5%; Score 6; DB 15; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      8 EGKDP 13
      |||||
Db     20 EGKDP 25

```

```

RESULT 13
US-09-367-528A-1
; Sequence 1, Application US/09367528A
; Publication No. US20010051359A1
; GENERAL INFORMATION:
; APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
; TITLE OF INVENTION: Geranyl Diphosphate Synthetase Gene
; FILE REFERENCE: PH-586
; CURRENT APPLICATION NUMBER: US/09/367,528A
; PRIOR FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: JP97/346686
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: 82
; OTHER INFORMATION: Xaa represents Val, Leu, Ile, Thr, Asp, Glu, Asn, Gln, Lys,
; OTHER INFORMATION: Arg, Cys, Met, Phe, Tyr, Trp, His or Pro.
US-09-367-528A-1

```

```

Query Match      37.5%; Score 6; DB 9; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      9 GKDP 14
      |||||
Db     62 GKDP 67

```

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RESULT 14
US-09-367-528A-3
; Sequence 3, Application US/09367528A

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; Publication No. US20010051359A1
; GENERAL INFORMATION:
; APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
; TITLE OF INVENTION: Geranyl Diphosphate Synthetase Gene
; FILE REFERENCE: PH-586
; CURRENT APPLICATION NUMBER: US/09/367,528A
; PRIOR FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: JP97/346686
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-09-367-528A-3

```

```

Query Match      37.5%; Score 6; DB 9; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      9 GKDP 14
      |||||
Db     62 GKDP 67

```

```

RESULT 15
US-09-367-528A-5
; Sequence 5, Application US/09367528A
; Publication No. US20010051359A1
; GENERAL INFORMATION:
; APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
; TITLE OF INVENTION: Geranyl Diphosphate Synthetase Gene
; FILE REFERENCE: PH-586
; CURRENT APPLICATION NUMBER: US/09/367,528A
; PRIOR FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: JP97/346686
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-09-367-528A-5

```

```

Query Match      37.5%; Score 6; DB 9; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      9 GKDP 14
      |||||
Db     62 GKDP 67

```

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Search completed: July 27, 2005, 19:27:28
Job time : 8.88889 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 27, 2005, 19:16:56 ; Search time 42.4533 Seconds
(without alignments)
616.687 Million cell updates/sec

Title: US-10-030-937-68
Perfect score: 94
Sequence: 1 FSWDNCPEGKDPVIR 16

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cgn2_1/USPTO spo01/US10030937/runat 26072005 132236 10399/app query.fasta_1.789
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	53	56.4	35417	4	US-09-949-016-16129
c 2	53	56.4	49052	4	US-09-949-016-12203
3	51	54.3	561	4	US-09-489-039A-2692
4	50.5	53.7	45197	4	US-09-949-016-16208
5	50.5	53.7	254405	4	US-09-949-016-14381
c 6	49	52.1	240157	4	US-09-949-016-16264
7	48	51.1	4200	1	US-07-841-654B-1
8	48	51.1	4200	1	US-07-946-234A-1
9	48	51.1	4200	1	US-08-123-161A-1
10	48	51.1	4200	1	US-08-483-278-1
11	48	51.1	4200	5	PCT-US93-01560-1
c 12	47	50.0	3647	4	US-09-949-016-2641

c 13	47	50.0	54950	4	US-09-949-016-14383	Sequence 14383, A
14	46.5	49.5	12416	4	US-09-949-016-12000	Sequence 12000, A
15	46.5	49.5	12418	4	US-09-949-016-16170	Sequence 16170, A
c 16	46	48.9	6409	4	US-09-967-908A-1	Sequence 1, Appli
c 17	46	48.9	6409	4	US-10-159-151-1	Sequence 1, Appli
18	46	48.9	17644	4	US-09-949-016-16342	Sequence 16342, A
19	46	48.9	17645	4	US-09-949-016-11805	Sequence 11805, A
20	46	48.9	17645	4	US-09-949-016-14188	Sequence 14188, A
21	46	48.9	44019	4	US-09-949-016-14902	Sequence 14902, A
c 22	46	48.9	640681	4	US-09-790-988-1	Sequence 1, Appli
23	45	47.9	3940	4	US-09-976-594-573	Sequence 573, App
24	45	47.9	28720	3	US-09-341-587-7	Sequence 7, Appli
25	45	47.9	42975	4	US-09-949-016-11965	Sequence 11965, A
26	45	47.9	115814	4	US-09-949-016-16205	Sequence 16205, A
27	45	47.9	218940	4	US-09-949-016-17539	Sequence 17539, A
c 28	45	47.9	275110	4	US-09-949-016-12706	Sequence 12706, A
c 29	45	47.9	275110	4	US-09-949-016-16070	Sequence 16070, A
30	45	47.9	1230025	4	US-09-198-452A-1	Sequence 1, Appli
31	45	47.9	1230230	4	US-09-438-185A-1	Sequence 1, Appli
32	44	46.8	601	4	US-09-949-016-25462	Sequence 25462, A
33	44	46.8	601	4	US-09-949-016-25463	Sequence 25463, A
34	44	46.8	601	4	US-09-949-016-25464	Sequence 25464, A
35	44	46.8	601	4	US-09-949-016-25465	Sequence 25465, A
36	44	46.8	601	4	US-09-949-016-25466	Sequence 25466, A
37	44	46.8	601	4	US-09-949-016-48513	Sequence 48513, A
38	44	46.8	601	4	US-09-949-016-73632	Sequence 73632, A
39	44	46.8	601	4	US-09-949-016-73633	Sequence 73633, A
40	44	46.8	601	4	US-09-949-016-73634	Sequence 73634, A
41	44	46.8	601	4	US-09-949-016-73635	Sequence 73635, A
42	44	46.8	601	4	US-09-949-016-73636	Sequence 73636, A
43	44	46.8	1622	4	US-09-599-360B-48	Sequence 48, Appli
44	44	46.8	3271	4	US-09-548-797B-1	Sequence 1, Appli
45	44	46.8	3390	4	US-09-548-797B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-949-016-16129/c
; Sequence 16129, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16129
; LENGTH: 35417
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16129

Alignment Scores:
Pred. No.: 200 Length: 35417
Score: 53.00 Matches: 9
Percent Similarity: 66.67% Conservative: 1
Best Local Similarity: 60.00% Mismatches: 5
Query Match: 56.38% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-68 (1-16) x US-09-949-016-16129 (1-35417)

Qy 2 SerTrpAspAsnCysPheGluGlyAspProAlaValIleArg 16

US-09-949-016-14381

Alignment Scores:

Pred. No.:	6.47e+03	Length:	254405
Score:	50.50	Matches:	10
Percent Similarity:	68.42%	Conservative:	3
Best Local Similarity:	52.63%	Mismatches:	3
Query Match:	53.72%	Indels:	3
DB:	4	Gaps:	1

US-10-030-937-68 (1-16) x US-09-949-016-14381 (1-254405)

Qy 1 PheSerTrpAsp-----AsnCysPheGluGlyLysAspProAlaValIleArg 16

Db 45072 TTCTCTGGCACAGTATGATTTCCTGTTTCGAAGAAAAAACCCAGAGTTTAAAGA 45128

RESULT 6

US-09-949-016-16264/c

; Sequence 16264, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 16264

; LENGTH: 240157

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(240157)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-16264

Alignment Scores:

Pred. No.:	1.14e+04	Length:	240157
Score:	49.00	Matches:	7
Percent Similarity:	84.62%	Conservative:	4
Best Local Similarity:	53.85%	Mismatches:	2
Query Match:	52.13%	Indels:	0
DB:	4	Gaps:	0

US-10-030-937-68 (1-16) x US-09-949-016-16264 (1-240157)

Qy 1 PheSerTrpAspAsnCysPheGluGlyLysAspProAla 13

Db 80562 TTTTCTGGCCAGCTGCTTCAAGGCAGATATCCCTCA 80524

RESULT 7

US-07-841-654B-1

; Sequence 1, Application US/07841654B

; Patent No. 5260209

; GENERAL INFORMATION:

; APPLICANT: Campbell, Kevin P.

; APPLICANT: Ibraghimov-Beskrovnya, Oxana

; APPLICANT: Ervasti, James M.

; APPLICANT: Leveille, Cynthia J.

; APPLICANT: Matsumura, Kiichiro

; TITLE OF INVENTION: DNA ENCODING DYSTROPHIN-ASSOCIATED

; TITLE OF INVENTION: PROTEINS

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: MA

; COUNTRY: USA

; ZIP: 02173

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/841,654B

; FILING DATE: 19920220

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Brook, David E.

; REGISTRATION NUMBER: 22,592

; REFERENCE/DOCKET NUMBER: UIRF89-11AA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617 861-6240

; TELEFAX: 617 861-9540

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4200 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 170..2855

US-07-841-654B-1

Alignment Scores:

Pred. No.:	124	Length:	4200
Score:	48.00	Matches:	7
Percent Similarity:	75.00%	Conservative:	2
Best Local Similarity:	58.33%	Mismatches:	3
Query Match:	51.06%	Indels:	0
DB:	1	Gaps:	0

US-10-030-937-68 (1-16) x US-07-841-654B-1 (1-4200)

Qy 3 TrpAspAsnCysPheGluGlyLysAspProAlaVal 14

Db 73 TGGAGCAGGTGTGCAGAGGGTGAGGCCCGGCTCTG 108

RESULT 8

US-07-946-234A-1

; Sequence 1, Application US/07946234A

; Patent No. 5308752

; GENERAL INFORMATION:

; APPLICANT: Campbell, Kevin P.

; APPLICANT: Matsumura, Kiichiro

; TITLE OF INVENTION: DIAGNOSIS OF AUTOSOMAL MUSCULAR DYSTROPHY

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS

; STREET: 2 Militia Drive

; CITY: Lexington

; STATE: MA

; COUNTRY: US

; ZIP: 02173

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/946,234A

; FILING DATE: 19920914

; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: UIRF89-11AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)861-6240
TELEFAX: (617)861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4200 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 170..2855
US-07-946-234A-1
Alignment Scores:
Pred. No.: 124 Length: 4200
Score: 48.00 Matches: 7
Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 58.33% Mismatches: 3
Query Match: 51.06% Indels: 0
DB: 1 Gaps: 0
US-10-030-937-68 (1-16) x US-07-946-234A-1 (1-4200)
QY 3 TrpAspAsnCysPheGluGlyLysAspProAlaVal 14
Db 73 TGGAGCAGGTGTGCAGAGGGTGAGGACCCGGCTCTG 108
RESULT 9
US-08-123-161A-1
Sequence 1, Application US/08123161A
Patent No. 5449616
GENERAL INFORMATION:
APPLICANT: Campbell, Kevin P.
APPLICANT: Roberts, Steven L.
APPLICANT: Anderson, Richard D.
APPLICANT: Ibraghimov, Oxana B.
APPLICANT: Yang, Bin
TITLE OF INVENTION: NUCLEIC ACID ENCODING DYSTROPHIN-ASSOCIATED
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,161A
FILING DATE: 16-SEP-93
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/946,234
FILING DATE: 14-SEP-92
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: UIRF89-11A4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 4200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 170..2855
US-08-123-161A-1
Alignment Scores:
Pred. No.: 124 Length: 4200
Score: 48.00 Matches: 7
Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 58.33% Mismatches: 3
Query Match: 51.06% Indels: 0
DB: 1 Gaps: 0
US-10-030-937-68 (1-16) x US-08-123-161A-1 (1-4200)
QY 3 TrpAspAsnCysPheGluGlyLysAspProAlaVal 14
Db 73 TGGAGCAGGTGTGCAGAGGGTGAGGACCCGGCTCTG 108
RESULT 10
US-08-483-278-1
Sequence 1, Application US/08483278
Patent No. 5686073
GENERAL INFORMATION:
APPLICANT: Campbell, Kevin P.
APPLICANT: Ibraghimov, Oxana B.
APPLICANT: Ervasti, James M.
APPLICANT: Leveille, Cynthia J.
TITLE OF INVENTION: NUCLEIC ACID ENCODING DYSTROPHIN-ASSOCIATED
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,278
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,161
FILING DATE: 16-SEP-93
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: UIRF89-11A5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 170..2855

US-08-483-278-1
Alignment Scores:
Pred. No.: 124 Length: 4200
Score: 48.00 Matches: 7
Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 58.33% Mismatches: 3
Query Match: 51.06% Indels: 0
DB: 1 Gaps: 0

US-10-030-937-68 (1-16) x US-08-483-278-1 (1-4200)

Qy 3 TrpAspAsnCysPheGluGlyLysAspProAlaVal 14
||| |||||:|||||:|
Db 73 TGGAGCAGGTGTCAGAGGTTGAGGACCGGCTCTG 108

RESULT 11
PCT-US93-01560-1
; Sequence 1, Application PC/TUS9301560
; GENERAL INFORMATION:
; APPLICANT: University of Iowa Research Foundation
; TITLE OF INVENTION: DNA ENCODING DYSTROPHIN-ASSOCIATED
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01560
; FILING DATE: 19930219
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/841,654
; FILING DATE: 20-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: UIRF89-11AA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 861-6240
; TELEFAX: 617 861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4200 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 170..2855
PCT-US93-01560-1

Alignment Scores:
Pred. No.: 124 Length: 4200
Score: 48.00 Matches: 7
Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 58.33% Mismatches: 3
Query Match: 51.06% Indels: 0
DB: 5 Gaps: 0

US-10-030-937-68 (1-16) x PCT-US93-01560-1 (1-4200)

Qy 3 TrpAspAsnCysPheGluGlyLysAspProAlaVal 14

Db 73 TGGAGCAGGTGTCAGAGGTTGAGGACCGGCTCTG 108
||| ||| |||||:|||||:|
RESULT 12
US-09-949-016-2641/c
; Sequence 2641, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2641
; LENGTH: 3647
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2641

Alignment Scores:
Pred. No.: 159 Length: 3647
Score: 47.00 Matches: 7
Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 58.33% Mismatches: 3
Query Match: 50.00% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-68 (1-16) x US-09-949-016-2641 (1-3647)

Qy 3 TrpAspAsnCysPheGluGlyLysAspProAlaVal 14
||| |||||:|||||:|
Db 1836 TGGGATTGCTGTTTCCAAGGGGAAAAACCAATAGTG 1801

RESULT 13
US-09-949-016-14383/c
; Sequence 14383, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14383
; LENGTH: 54950
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(54950)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14383

Alignment Scores:
Pred. No.: 4.4e+03 Length: 54950

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Score: 47.00 Matches: 7
Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 58.33% Mismatches: 3
Query Match: 50.00% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-68 (1-16) x US-09-949-016-14383 (1-54950)

Qy 3 TrpAspAsnCysPheGluGlyLysAspProAlaVal 14
    ||||| ||||| :|||: |||
Db 51138 TGGGATTGCTGTTTCCAAGGGGAAAACCAATAGTG 51103
    ||||| ||||| :|||: |||

RESULT 14
US-09-949-016-12000
; Sequence 12000, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12000
; LENGTH: 12416
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12000

Alignment Scores:
Pred. No.: 882 Length: 12416
Score: 46.50 Matches: 9
Percent Similarity: 57.14% Conservative: 3
Best Local Similarity: 42.86% Mismatches: 4
Query Match: 49.47% Indels: 5
DB: 4 Gaps: 1

US-10-030-937-68 (1-16) x US-09-949-016-12000 (1-12416)

Qy 1 PheSerTrp-----AspAsnCysPheGluGlyLysAspProAlaVal 15
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Db 4414 TTCTCTGGTCCAGTTTACCTTTAGATAAATGTTTAAAGGGTAAATATGTGTATTCA 4473
    ||||| ||||| :|||: |||

Qy 16 Arg 16
    |||
Db 4474 AGA 4476

RESULT 15
US-09-949-016-16170
; Sequence 16170, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16170
; LENGTH: 12418
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16170

Alignment Scores:
Pred. No.: 883 Length: 12418
Score: 46.50 Matches: 9
Percent Similarity: 57.14% Conservative: 3
Best Local Similarity: 42.86% Mismatches: 4
Query Match: 49.47% Indels: 5
DB: 4 Gaps: 1

US-10-030-937-68 (1-16) x US-09-949-016-16170 (1-12418)

Qy 1 PheSerTrp-----AspAsnCysPheGluGlyLysAspProAlaVal 15
    ||||| ||||| :|||: |||
Db 4414 TTCTCTGGTCCAGTTTACCTTTAGATAAATGTTTAAAGGGTAAATATGTGTATTCA 4473
    ||||| ||||| :|||: |||

Qy 16 Arg 16
    |||
Db 4474 AGA 4476

Search completed: July 27, 2005, 19:40:42
Job time : 66.4533 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 12:32:19 ; Search time 3.12889 Seconds
(without alignments)
381.728 Million cell updates/sec

Title: US-10-030-937-72
Perfect score: 83
Sequence: 1 YSLPKSEFAVPDLELP 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	95.2	178	4 US-09-183-841-2	Sequence 2, Appli
2	79	95.2	193	4 US-09-183-841-1	Sequence 1, Appli
3	47	56.6	2710	2 US-08-568-459A-12	Sequence 12, Appl
4	47	56.6	2710	2 US-08-487-826B-12	Sequence 12, Appl
5	47	56.6	2710	3 US-09-210-288-12	Sequence 12, Appl
6	47	56.6	3060	2 US-08-487-826B-14	Sequence 14, Appl
7	44	53.0	307	4 US-09-543-681A-4241	Sequence 4241, Ap
8	43	51.8	471	3 US-08-911-853-4	Sequence 4, Appli
9	43	51.8	471	3 US-09-479-409-4	Sequence 4, Appli
10	43	51.8	471	3 US-09-479-453-4	Sequence 4, Appli
11	43	51.8	812	4 US-09-489-039A-14282	Sequence 14282, A
12	41	49.4	74	4 US-09-902-540-11402	Sequence 11402, A
13	41	49.4	186	4 US-09-107-532A-5213	Sequence 5213, Ap
14	41	49.4	226	4 US-09-107-532A-6759	Sequence 6759, Ap
15	41	49.4	366	4 US-09-252-991A-26920	Sequence 26920, A
16	41	49.4	510	3 US-08-948-564-4	Sequence 4, Appli
17	40.5	48.8	476	4 US-09-248-796A-20470	Sequence 20470, A
18	40	48.2	112	4 US-09-489-039A-14284	Sequence 14284, A
19	40	48.2	251	4 US-09-248-796A-19708	Sequence 19708, A
20	40	48.2	4536	4 US-09-180-422B-27	Sequence 27, Appl
21	40	48.2	4536	4 US-09-079-030-1	Sequence 1, Appli
22	40	48.2	4563	4 US-09-108-006C-1	Sequence 1, Appli
23	40	48.2	4563	4 US-09-538-092-842	Sequence 842, App
24	39.5	47.6	548	4 US-09-252-991A-21629	Sequence 21629, A
25	39	47.0	40	4 US-09-079-030-76	Sequence 76, Appl
26	39	47.0	580	4 US-09-489-039A-14205	Sequence 14205, A
27	39	47.0	776	4 US-09-252-991A-17570	Sequence 17570, A

28	39	47.0	900	4 US-09-107-532A-5284	Sequence 5284, Ap
29	38.5	46.4	233	3 US-09-094-148-2	Sequence 2, Appli
30	38	45.8	22	4 US-09-079-030-79	Sequence 79, Appl
31	38	45.8	337	4 US-09-252-991A-16766	Sequence 16766, A
32	38	45.8	349	4 US-09-270-767-42023	Sequence 42023, A
33	38	45.8	421	4 US-09-198-452A-535	Sequence 535, App
34	38	45.8	423	4 US-09-248-796A-19425	Sequence 19425, A
35	38	45.8	429	4 US-09-438-185A-497	Sequence 497, App
36	38	45.8	433	4 US-09-538-092-1088	Sequence 1088, Ap
37	38	45.8	442	4 US-09-949-016-11671	Sequence 11671, A
38	38	45.8	537	3 US-08-886-886-17	Sequence 17, Appl
39	38	45.8	547	4 US-09-107-532A-5905	Sequence 5905, Ap
40	38	45.8	564	4 US-09-543-681A-6932	Sequence 6932, Ap
41	38	45.8	697	2 US-08-674-351-4	Sequence 4, Appli
42	38	45.8	840	4 US-09-079-030-214	Sequence 214, App
43	37.5	45.2	170	4 US-09-252-991A-29833	Sequence 29833, A
44	37.5	45.2	454	3 US-09-134-001C-4853	Sequence 4853, Ap
45	37.5	45.2	957	4 US-09-949-016-6154	Sequence 6154, Ap

ALIGNMENTS

RESULT 1
US-09-183-841-2
; Sequence 2, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanz0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: His tag at residues 1 to 17
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence of GM2 protein using His6 tag
US-09-183-841-2

Query Match 95.2%; Score 79; DB 4; Length 178;
Best Local Similarity 93.8%; Pred. No. 1.7e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSLPKSEFAVPDLELP 16
|||
Db 130 YSLPKSEFVVPDLELP 145

RESULT 2
US-09-183-841-1
; Sequence 1, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanz0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL

```

; LOCATION: (33)..(55)
; FEATURE:
; OTHER INFORMATION: residues 56-63 are included in a further precursor
; OTHER INFORMATION: form of the protein
US-09-183-841-1
Query Match          95.2%; Score 79; DB 4; Length 193;
Best Local Similarity 93.8%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSLPKSEFAVPDLELP 16
    ||||| |||||
Db 145 YSLPKSEFVVPDLELP 160

RESULT 3
US-08-568-459A-12
; Sequence 12, Application US/08568459A
; Patent No. 5849306
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellem, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,459A
; FILING DATE: 07-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2710 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
; US-08-568-459A-12

Query Match          56.6%; Score 47; DB 2; Length 2710;
Best Local Similarity 64.3%; Pred. No. 28;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 LPKSEFAVPDLELP 16
    ||||| |||||
Db 2121 LPKNDGTVPDLEKP 2134

US-09-183-841-1
Query Match          95.2%; Score 79; DB 4; Length 193;
Best Local Similarity 93.8%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSLPKSEFAVPDLELP 16
    ||||| |||||
Db 145 YSLPKSEFVVPDLELP 160

RESULT 3
US-08-568-459A-12
; Sequence 12, Application US/08568459A
; Patent No. 5849306
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellem, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,459A
; FILING DATE: 07-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2710 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
; US-08-568-459A-12

Query Match          56.6%; Score 47; DB 2; Length 2710;
Best Local Similarity 64.3%; Pred. No. 28;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 LPKSEFAVPDLELP 16
    ||||| |||||
Db 2121 LPKNDGTVPDLEKP 2134

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RESULT 4
US-08-487-826B-12
; Sequence 12, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellem, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2710 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
; US-08-487-826B-12

Query Match          56.6%; Score 47; DB 2; Length 2710;
Best Local Similarity 64.3%; Pred. No. 28;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 LPKSEFAVPDLELP 16
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Db 2121 LPKNDGTVPDLEKP 2134

RESULT 5
US-09-210-288-12
; Sequence 12, Application US/09210288
; Patent No. 6392026
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellem, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:

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;; ADDRESSEE: Knobbe Martens Olson & Bear
;; STREET: 620 Newport Center Drive 16th Floor
;; CITY: Newport Beach
;; STATE: California
;; COUNTRY: US
;; ZIP: 92660
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/210,288
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fuller, Michael
;; REGISTRATION NUMBER: 36,516
;; REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 235-8550
;; TELEFAX: (619) 235-0176
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2710 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Plasmodium falciparum
;; US-09-210-288-12

Query Match 56.6%; Score 47; DB 3; Length 2710;
Best Local Similarity 64.3%; Pred. No. 28;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 LPKSEFAVPDLPL 16
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Db 2121 LPRNDGTVPDLKP 2134

RESULT 6

US-08-487-826B-14
;; Sequence 14, Application US/08487826B
;; Patent No. 5993827
;; GENERAL INFORMATION:
;; APPLICANT: Sim, Kim L.
;; APPLICANT: Chitnis, Chetan
;; APPLICANT: Miller, Louis H.
;; APPLICANT: Peterson, David S.
;; APPLICANT: Su, Xin-zhaun
;; APPLICANT: Wellem, Thomas E.
;; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
;; AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
;; NUMBER OF SEQUENCES: 45
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Knobbe Martens Olson & Bear
;; STREET: 620 Newport Center Drive 16th Floor
;; CITY: Newport Beach
;; STATE: California
;; COUNTRY: US
;; ZIP: 92660
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/487,826B
;; FILING DATE: 10-SEP-1993
;; CLASSIFICATION: 435

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Israelsen, Ned
;; REGISTRATION NUMBER: 29,655
;; REFERENCE/DOCKET NUMBER: NIH121.001CP1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 235-8550
;; TELEFAX: (619) 235-0176
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3060 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-487-826B-14

Query Match 56.6%; Score 47; DB 2; Length 3060;
Best Local Similarity 64.3%; Pred. No. 33;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 LPKSEFAVPDLPL 16
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Db 2119 LPRNDGTVPDLKP 2132

RESULT 7

US-09-543-681A-4241
;; Sequence 4241, Application US/09543681A
;; Patent No. 6605709
;; GENERAL INFORMATION:
;; APPLICANT: GARY BRETON

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
;; AND THERAPEUTICS
;; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: 2709.1002-001
;; CURRENT APPLICATION NUMBER: US/09/543,681A
;; CURRENT FILING DATE: 2000-04-05
;; PRIOR APPLICATION NUMBER: US 60/128,706
;; PRIOR FILING DATE: 1999-04-09
;; NUMBER OF SEQ ID NOS: 8344
;; SEQ ID NO 4241
;; LENGTH: 307
;; TYPE: PRT

;; ORGANISM: Proteus mirabilis
;; US-09-543-681A-4241

Query Match 53.0%; Score 44; DB 4; Length 307;
Best Local Similarity 50.0%; Pred. No. 6.9;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 YSLPKSEFAVPDL 14
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Db 220 YSLPQPQTDPDIQ 233

RESULT 8

US-08-911-853-4
;; Sequence 4, Application US/08911853
;; Patent No. 6048710
;; GENERAL INFORMATION:
;; APPLICANT: Gerritse, Gijbert
;; APPLICANT: Quax, Wilhelmus J.
;; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
;; EXPRESSION LEVELS
;; NUMBER OF SEQUENCES: 37
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genencor International
;; STREET: 925 Page Mill Road
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304-1013
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette

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; ; COMPUTER: IBM Compatible
; ; OPERATING SYSTEM: DOS
; ; SOFTWARE: FastSEQ for Windows Version 2.0
; ; CURRENT APPLICATION DATA:
; ; APPLICATION NUMBER: US/08/911,853
; ; FILING DATE:
; ; PRIOR APPLICATION DATA:
; ; APPLICATION NUMBER: 08/699,092
; ; FILING DATE: 16-AUG-1996
; ; ATTORNEY/AGENT INFORMATION:
; ; NAME: Glaister, Debra J
; ; REGISTRATION NUMBER: 33,888
; ; REFERENCE/DOCKET NUMBER: GC361-2
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: 650-846-7620
; ; TELEFAX: 650-845-6504
; ; INFORMATION FOR SEQ ID NO: 4:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 471 amino acids
; ; TYPE: amino acid
; ; STRANDEDNESS: single
; ; TOPOLOGY: linear
; ; US-08-911-853-4

Query Match 51.8%; Score 43; DB 3; Length 471;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 YSLPKSEFAVPDLPLP 16
Db 41 YSIPTFDLVVSDLRLP 56

RESULT 9
US-09-479-409-4
; Sequence 4, Application US/09479409
; Patent No. 6225106
; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gijlsbert
; APPLICANT: Quax, Wilhelms J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,409
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; ;
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; ; TOPOLOGY: linear
; ; US-09-479-409-4

Query Match 51.8%; Score 43; DB 3; Length 471;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 YSLPKSEFAVPDLPLP 16
Db 41 YSIPTFDLVVSDLRLP 56

RESULT 10
US-09-479-453-4
; Sequence 4, Application US/09479453
; Patent No. 6313283
; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gijlsbert
; APPLICANT: Quax, Wilhelms J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,453
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ; US-09-479-453-4

Query Match 51.8%; Score 43; DB 3; Length 471;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 YSLPKSEFAVPDLPLP 16
Db 41 YSIPTFDLVVSDLRLP 56

RESULT 11
US-09-489-039A-14282
; Sequence 14282, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; ;
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; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 14282
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14282

Query Match          51.8%; Score 43; DB 4; Length 812;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      5 KSEFAVPDLELP 16
Db      762 KADFRVPPLLELP 773

RESULT 12
US-09-902-540-11402
; Sequence 11402, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11402
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11402

Query Match          49.4%; Score 41; DB 4; Length 74;
Best Local Similarity 43.8%; Pred. No. 4.2;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy      1 YSLPKSEFAVPDLELP 16
Db      23 YRLPEAMAAIPELQNP 38

RESULT 13
US-09-107-532A-5213
; Sequence 5213, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
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; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5213:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 186 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...186
; SEQUENCE DESCRIPTION: SEQ ID NO: 5213:
US-09-107-532A-5213

Query Match          49.4%; Score 41; DB 4; Length 186;
Best Local Similarity 64.3%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 SLPKSEFAVPDLEL 15
Db      37 SLPFSRFAAPDCAL 50

RESULT 14
US-09-107-532A-6759
; Sequence 6759, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
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; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6759:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 226 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
;   ORGANISM: Enterococcus faecium
; FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (B) LOCATION 1...226
; SEQUENCE DESCRIPTION: SEQ ID NO: 6759:
US-09-107-532A-6759

Query Match          49.4%; Score 41; DB 4; Length 226;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      2 SLPKSEFAVPDL 13
Db      196 NLPSEYVIPDL 207

RESULT 15
US-09-252-991A-26920
; Sequence 26920, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26920
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26920

Query Match          49.4%; Score 41; DB 4; Length 366;
Best Local Similarity 43.8%; Pred. No. 30;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy      1 YSLPKSEFAVPDL 16
Db      186 YTIPTFDMVVDLRLP 201

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Job time : 4.12889 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 18:09:01 ; Search time 35.0578 Seconds

(without alignments)
177.532 Million cell updates/sec

Title: US-10-030-937-72

Perfect score: 83

Sequence: 1 YSLPKSEFAVPDLPLP 16

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications_AA:**

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
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- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	79	95.2	193	15	US-10-170-385-389 Sequence 389, App
2	79	95.2	193	16	US-10-723-860-529 Sequence 529, App
3	49	59.0	894	17	US-10-732-923-8428 Sequence 8428, App
4	47	56.6	2710	13	US-10-153-273-12 Sequence 12, Appl
5	44.5	53.6	120	15	US-10-424-599-284187 Sequence 284187,
6	44	53.0	328	15	US-10-369-493-4173 Sequence 4173, Ap
7	44	53.0	329	15	US-10-320-797-3110 Sequence 3110, Ap
8	43.5	52.4	1383	14	US-10-021-955-82 Sequence 82, Appl
9	43.5	52.4	1383	14	US-10-021-955-86 Sequence 86, Appl
10	43.5	52.4	1383	14	US-10-021-955-87 Sequence 87, Appl
11	43.5	52.4	1389	14	US-10-021-955-79 Sequence 79, Appl

12	43	51.8	183	16	US-10-425-115-261209 Sequence 261209,
13	43	51.8	828	15	US-10-282-122A-60144 Sequence 60144, A
14	42.5	51.2	104	16	US-10-425-115-194142 Sequence 194142,
15	42.5	51.2	1391	14	US-10-021-955-85 Sequence 85, Appl
16	42.5	51.2	1398	16	US-10-408-765A-1007 Sequence 1007, Ap
17	42.5	51.2	1461	10	US-09-940-227-77 Sequence 77, Appl
18	42.5	51.2	1461	14	US-10-021-955-88 Sequence 88, Appl
19	42.5	51.2	1461	15	US-10-467-433-10 Sequence 10, Appl
20	42.5	51.2	1461	15	US-10-332-947-30 Sequence 30, Appl
21	42.5	51.2	1461	17	US-10-933-058-77 Sequence 77, Appl
22	42.5	51.2	1483	15	US-10-332-947-29 Sequence 29, Appl
23	42.5	51.2	1549	15	US-10-363-616-314 Sequence 314, App
24	42	50.6	63	16	US-10-425-115-232729 Sequence 232729,
25	42	50.6	140	16	US-10-425-115-208031 Sequence 208031,
26	42	50.6	188	11	US-09-801-944B-234 Sequence 234, App
27	42	50.6	199	15	US-10-282-122A-65806 Sequence 65806, A
28	42	50.6	300	15	US-10-425-114-69294 Sequence 69294, A
29	42	50.6	393	15	US-10-282-122A-55243 Sequence 55243, A
30	42	50.6	852	16	US-10-437-963-204585 Sequence 204585,
31	42	50.6	1040	16	US-10-437-963-140470 Sequence 140470,
32	42	50.6	1127	16	US-10-437-963-140467 Sequence 140467,
33	42	50.6	1441	17	US-10-732-923-1652 Sequence 1652, Ap
34	42	50.6	1441	17	US-10-732-923-1653 Sequence 1653, Ap
35	41.5	50.0	186	15	US-10-425-114-39728 Sequence 39728, A
36	41.5	50.0	313	15	US-10-424-599-235166 Sequence 235166,
37	41	49.4	68	16	US-10-437-963-136391 Sequence 136391,
38	41	49.4	85	16	US-10-425-115-356159 Sequence 356159,
39	41	49.4	102	16	US-10-437-963-107307 Sequence 107307,
40	41	49.4	106	16	US-10-425-115-321334 Sequence 321334,
41	41	49.4	153	15	US-10-425-114-61811 Sequence 61811, A
42	41	49.4	159	16	US-10-425-115-224622 Sequence 224622,
43	41	49.4	187	16	US-10-425-115-208030 Sequence 208030,
44	41	49.4	267	16	US-10-425-115-208027 Sequence 208027,
45	41	49.4	337	15	US-10-369-493-19438 Sequence 19438, A

ALIGNMENTS

RESULT 1

US-10-170-385-389
; Sequence 389, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-385-389

Query Match 95.2%; Score 79; DB 15; Length 193;
Best Local Similarity 93.8%; Pred. No. 5e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 YSLPKSEFAVPDLELP 16
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Db      145 YSLPKSEFVVPDLELP 160

RESULT 2
US-10-723-860-529
; Sequence 529, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 529
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-529

Query Match      95.2%; Score 79; DB 16; Length 193;
Best Local Similarity 93.8%; Pred. No. 5e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 YSLPKSEFAVPDLELP 16
      ||||||| |||||||
Db      145 YSLPKSEFVVPDLELP 160

RESULT 3
US-10-732-923-8428
; Sequence 8428, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 8428
; LENGTH: 894
; TYPE: PRT
; ORGANISM: Oryza sativa (japonica cultivar-group)
US-10-732-923-8428

Query Match      59.0%; Score 49; DB 17; Length 894;
Best Local Similarity 61.5%; Pred. No. 30;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      3 LPKSEFAVPDLEL 15
      :||| :|||||
Db      817 VPRSEISPDLEL 829

RESULT 4
US-10-153-273-12
; Sequence 12, Application US/10153273
; Publication No. US20020169305A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
```

```
;
; Miller, Louis H.
; Peterson, David S.
; Su, Xin-zhaun
; Welles, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
;
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,273
; FILING DATE: 21-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,288
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
;
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2710 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-153-273-12

Query Match      56.6%; Score 47; DB 13; Length 2710;
Best Local Similarity 64.3%; Pred. No. 2.3e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 LPKSEFAVPDLELP 16
      |||:: |||||
Db      2121 LPKNDGTVPDLEKP 2134

RESULT 5
US-10-424-599-284187
; Sequence 284187, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 284187
; LENGTH: 120
; TYPE: PRT
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; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_98646C.1.pep
US-10-424-599-284187

Query Match      53.6%; Score 44.5; DB 15; Length 120;
Best Local Similarity 68.8%; Pred. No. 17;
Matches 11; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY      1 YSLPKSEFAVPDLELP 16
Db      98 YFLPLSE-SEPDLELP 112

RESULT 6
US-10-369-493-4173
; Sequence 4173, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4173
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Neurospora crassa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(328)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-4173

Query Match      53.0%; Score 44; DB 15; Length 328;
Best Local Similarity 61.5%; Pred. No. 65;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      4 PKSEFAVPDLELP 16
Db      105 PKAEWXYPTLSLP 117

RESULT 7
US-10-320-797-3110
; Sequence 3110, Application US/10320797
; Publication No. US20040014955A1
; GENERAL INFORMATION:
; APPLICANT: Eroshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3110
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-10-320-797-3110

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Query Match      53.0%; Score 44; DB 15; Length 329;
Best Local Similarity 56.2%; Pred. No. 65;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 YSLPKSEFAVPDLELP 16
Db      58 FSLPVKBFQIIDLFLP 73

RESULT 8
US-10-021-955-82
; Sequence 82, Application US/10021955
; Publication No. US20030039987A1
; GENERAL INFORMATION:
; APPLICANT: Lupski, James R
; APPLICANT: Boerkoel, Cornelius F
; APPLICANT: Takashima, Hiroshi
; TITLE OF INVENTION: Defects in Periaxin Associated with Myelinopathies
; FILE REFERENCE: P02086USI/10026309
; CURRENT APPLICATION NUMBER: US/10/021,955
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: US 60/255,217
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 1383
; TYPE: PRT
; ORGANISM: Rat
US-10-021-955-82

Query Match      52.4%; Score 43.5; DB 14; Length 1383;
Best Local Similarity 60.0%; Pred. No. 4e+02;
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY      3 LPKS-EFAVPDLELP 16
Db      453 LPKAPEAAIPDVQLP 467

RESULT 9
US-10-021-955-86
; Sequence 86, Application US/10021955
; Publication No. US20030039987A1
; GENERAL INFORMATION:
; APPLICANT: Lupski, James R
; APPLICANT: Boerkoel, Cornelius F
; APPLICANT: Takashima, Hiroshi
; TITLE OF INVENTION: Defects in Periaxin Associated with Myelinopathies
; FILE REFERENCE: P02086USI/10026309
; CURRENT APPLICATION NUMBER: US/10/021,955
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: US 60/255,217
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 1383
; TYPE: PRT
; ORGANISM: Rat
US-10-021-955-86

Query Match      52.4%; Score 43.5; DB 14; Length 1383;
Best Local Similarity 60.0%; Pred. No. 4e+02;
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY      3 LPKS-EFAVPDLELP 16
Db      453 LPKAPEAAIPDVQLP 467

RESULT 10
US-10-021-955-87

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; Sequence 87, Application US/10021955
; Publication No. US20030039987A1
; GENERAL INFORMATION:
; APPLICANT: Lupski, James R
; APPLICANT: Boerkoel, Cornelius F
; APPLICANT: Takashima, Hiroshi
; TITLE OF INVENTION: Defects in Periaxin Associated with Myelinopathies
; FILE REFERENCE: P02086USI/10026309
; CURRENT APPLICATION NUMBER: US/10/021,955
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: US 60/255,217
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 1383
; TYPE: PRT
; ORGANISM: Rat
US-10-021-955-87

Query Match      52.4%; Score 43.5; DB 14; Length 1383;
Best Local Similarity 60.0%; Pred. No. 4e+02;
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY      3 LPKS-EFAVPDLELP 16
      |||: |||: |||: |||
Db      453 LPKAPEAAIPDVQLP 467

RESULT 11
US-10-021-955-79
; Sequence 79, Application US/10021955
; Publication No. US20030039987A1
; GENERAL INFORMATION:
; APPLICANT: Lupski, James R
; APPLICANT: Boerkoel, Cornelius F
; APPLICANT: Takashima, Hiroshi
; TITLE OF INVENTION: Defects in Periaxin Associated with Myelinopathies
; FILE REFERENCE: P02086USI/10026309
; CURRENT APPLICATION NUMBER: US/10/021,955
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: US 60/255,217
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 1389
; TYPE: PRT
; ORGANISM: Rat
US-10-021-955-79

Query Match      52.4%; Score 43.5; DB 14; Length 1389;
Best Local Similarity 60.0%; Pred. No. 4.1e+02;
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY      3 LPKS-EFAVPDLELP 16
      |||: |||: |||: |||
Db      453 LPKAPEAAIPDVQLP 467

RESULT 12
US-10-425-115-261209
; Sequence 261209, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 261209
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_169837C.1.pep
US-10-425-115-261209

Query Match      51.8%; Score 43; DB 16; Length 183;
Best Local Similarity 72.7%; Pred. No. 49;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 SLPKSEFAVPD 12
      |||: |||: |||
Db      25 SLPRSSFPVPD 35

RESULT 13
US-10-282-122A-60144
; Sequence 60144, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60144
; LENGTH: 828
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-10-282-122A-60144

Query Match      51.8%; Score 43; DB 15; Length 828;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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Qy 5 KSEFAVPDLELP 16
|::|||
Db 758 KADFRVPDLELP 769

RESULT 14
US-10-425-115-194142
; Sequence 194142, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 194142
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_108637C.1.pep
US-10-425-115-194142

Query Match 51.2%; Score 42.5; DB 16; Length 104;
Best Local Similarity 38.1%; Pred. No. 31;
Matches 8; Conservative 5; Mismatches 3; Indels 5; Gaps 1;

Qy 1 YSLPKSEFA-----VPDLELP 16
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Db 64 FEIPPEYSHNTIIVPDPEIP 84

RESULT 15
US-10-021-955-85
; Sequence 85, Application US/10021955
; Publication No. US20030039987A1
; GENERAL INFORMATION:
; APPLICANT: Lupeki, James R
; APPLICANT: Boerkoel, Cornelius F
; APPLICANT: Takashima, Hiroshi
; TITLE OF INVENTION: Defects in Periaxin Associated with Myelinopathies
; FILE REFERENCE: P02086USI/10026309
; CURRENT APPLICATION NUMBER: US/10/021,955
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: US 60/255,217
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
; LENGTH: 1391
; TYPE: PRT
; ORGANISM: Mouse
US-10-021-955-85

Query Match 51.2%; Score 42.5; DB 14; Length 1391;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 10; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 3 LPK-SEFAVPDLELP 16
||| |
Db 510 LPKPENAVPDVHLP 524

Search completed: July 27, 2005, 19:16:51
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OM protein - protein search, using sw model

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Title: US-10-030-937-72
Perfect score: 16
Sequence: 1 YSLPKSEFAVPDLPLP 16

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Gapop 60.0 , Gapext 60.0

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Total number of hits satisfying chosen parameters: 513545

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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	50.0	178	US-09-183-841-2	Sequence 2, Appli
2	8	50.0	193	US-09-183-841-1	Sequence 1, Appli
3	6	37.5	55	US-09-270-767-62426	Sequence 52426, A
4	6	37.5	112	US-09-489-039A-14284	Sequence 14284, A
5	6	37.5	219	US-09-248-796A-16515	Sequence 16515, A
6	6	37.5	223	US-09-543-681A-7057	Sequence 7057, Ap
7	6	37.5	253	US-09-583-110-3681	Sequence 3681, Ap
8	6	37.5	255	US-08-778-717-11	Sequence 11, Appl
9	6	37.5	257	US-08-778-717-13	Sequence 13, Appl
10	6	37.5	258	US-09-543-681A-8135	Sequence 8135, Ap
11	6	37.5	284	US-09-107-433-4311	Sequence 4311, Ap
12	6	37.5	309	US-09-902-540-13383	Sequence 13383, A
13	6	37.5	329	US-09-719-108-6	Sequence 6, Appli
14	6	37.5	349	US-09-270-767-42023	Sequence 42023, A
15	6	37.5	356	US-09-270-767-46804	Sequence 46804, A
16	6	37.5	473	US-09-252-991A-23441	Sequence 23441, A
17	6	37.5	534	US-09-134-000C-5087	Sequence 5087, Ap
18	6	37.5	537	US-08-886-886-17	Sequence 17, Appl
19	6	37.5	547	US-09-107-532A-5905	Sequence 5905, Ap
20	6	37.5	580	US-09-489-039A-14205	Sequence 14205, A
21	6	37.5	834	US-09-252-991A-17616	Sequence 17616, A
22	6	37.5	2329	US-08-755-587-16	Sequence 16, Appl
23	6	37.5	2451	US-09-949-016-9675	Sequence 9675, Ap
24	6	37.5	2618	US-09-413-814-28	Sequence 28, Appl
25	6	37.5	3418	US-08-639-501-2	Sequence 2, Appli
26	6	37.5	3418	US-08-603-753D-4	Sequence 4, Appli
27	6	37.5	3418	US-09-044-946-2	Sequence 2, Appli

28	6	37.5	3418	3	US-08-755-587-44	Sequence 44, Appl
29	6	37.5	3418	3	US-09-044-908-2	Sequence 2, Appli
30	6	37.5	3418	3	US-09-099-753-4	Sequence 4, Appli
31	6	37.5	3418	3	US-08-986-106-4	Sequence 4, Appli
32	5	31.2	6	1	US-08-467-607-12	Sequence 12, Appl
33	5	31.2	6	2	US-08-469-362-12	Sequence 12, Appl
34	5	31.2	6	2	US-08-850-392-12	Sequence 12, Appl
35	5	31.2	11	3	US-09-476-482-11	Sequence 11, Appl
36	5	31.2	15	3	US-08-946-026-57	Sequence 57, Appl
37	5	31.2	19	2	US-08-793-490-5	Sequence 5, Appli
38	5	31.2	20	1	US-08-467-607-4	Sequence 4, Appli
39	5	31.2	20	2	US-08-469-362-4	Sequence 4, Appli
40	5	31.2	20	2	US-08-850-392-4	Sequence 4, Appli
41	5	31.2	21	3	US-09-406-781-40	Sequence 40, Appl
42	5	31.2	21	4	US-09-880-132-40	Sequence 40, Appl
43	5	31.2	35	3	US-09-079-372-11	Sequence 11, Appl
44	5	31.2	48	4	US-09-205-258-574	Sequence 574, App
45	5	31.2	54	4	US-09-640-211A-2293	Sequence 2293, Ap

ALIGNMENTS

RESULT 1
US-09-183-841-2
; Sequence 2, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanz0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: His tag at residues 1 to 17
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence of GM2 protein using His6 tag
US-09-183-841-2

Query Match 50.0%; Score 8; DB 4; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSLPKSEF 8
|||||
Db 130 YSLPKSEF 137

RESULT 2
US-09-183-841-1
; Sequence 1, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanz0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL

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; LOCATION: (33)..(55)
; FEATURE:
; OTHER INFORMATION: residues 56-63 are included in a further precursor
; OTHER INFORMATION: form of the protein
US-09-183-841-1

Query Match      50.0%; Score 8; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YSLPKSEF 8
      |||||
Db     145 YSLPKSEP 152

RESULT 3
US-09-270-767-62426
; Sequence 62426, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62426
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-62426

Query Match      37.5%; Score 6; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SLPKSE 7
      |||||
Db     32 SLPKSE 37

RESULT 4
US-09-489-039A-14284
; Sequence 14284, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 14284
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14284

Query Match      37.5%; Score 6; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 FAVPDL 13
      |||||
Db     107 FAVPDL 112
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RESULT 5
US-09-248-796A-16515
; Sequence 16515, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16515
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16515

Query Match      37.5%; Score 6; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 KSEFAV 10
      |||||
Db     207 KSEFAV 212

RESULT 6
US-09-543-681A-7057
; Sequence 7057, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7057
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7057

Query Match      37.5%; Score 6; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 EFAVPD 12
      |||||
Db     117 EFAVPD 122

RESULT 7
US-09-583-110-3681
; Sequence 3681, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
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; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3681
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3681

Query Match      37.5%; Score 6; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 KSEFAV 10
      |||||
Db      43 KSEFAV 48

RESULT 8
US-08-778-717-11
; Sequence 11, Application US/08778717
; Patent No. 6602689
; GENERAL INFORMATION:
; APPLICANT: UENO, EIICHI
; APPLICANT: NOBUYUKI, FUJII
; APPLICANT: OKADA, MASAHISA
; TITLE OF INVENTION: FUSED DNA SEQUENCE, FUSED PROTEIN
; TITLE OF INVENTION: EXPRESSED FROM SAID FUSED DNA SEQUENCE AND METHOD FOR
; TITLE OF INVENTION: EXPRESSING SAID DNA SEQUENCE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/778,717
; FILING DATE: 12-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 352225/1995
; FILING DATE: 28-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 2084-031-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: RECOMBINANT
; PUBLICATION INFORMATION:
; AUTHORS: NOBUYUKI FUJII ET AL,
; TITLE: FUSED DNA SEQUENCE, FUSED PROTEIN EXPRESSED
; TITLE: FROM SAID FUSED DNA SEQUENCE AND METHOD OF
; TITLE: EXPRESSING SAID FUSED PROTEIN

; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3681
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3681

Query Match      37.5%; Score 6; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 KSEFAV 10
      |||||
Db      43 KSEFAV 48

RESULT 9
US-08-778-717-13
; Sequence 13, Application US/08778717
; Patent No. 6602689
; GENERAL INFORMATION:
; APPLICANT: UENO, EIICHI
; APPLICANT: NOBUYUKI, FUJII
; APPLICANT: OKADA, MASAHISA
; TITLE OF INVENTION: FUSED DNA SEQUENCE, FUSED PROTEIN
; TITLE OF INVENTION: EXPRESSED FROM SAID FUSED DNA SEQUENCE AND METHOD FOR
; TITLE OF INVENTION: EXPRESSING SAID DNA SEQUENCE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/778,717
; FILING DATE: 12-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 352225/1995
; FILING DATE: 28-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 2084-031-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: RECOMBINANT
; PUBLICATION INFORMATION:
; AUTHORS: NOBUYUKI FUJII ET AL,
; TITLE: FUSED DNA SEQUENCE, FUSED PROTEIN EXPRESSED
; TITLE: FROM SAID FUSED DNA SEQUENCE AND METHOD OF
; TITLE: EXPRESSING SAID FUSED PROTEIN
; RELEVANT RESIDUES IN SEQ ID NO: 13: FROM 1 TO 257
US-08-778-717-13

Query Match      37.5%; Score 6; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 SEFAVP 11
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Db      77 SEFAVP 82
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Db 77 SEFAVP 82
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RESULT 10
US-09-543-681A-8135
; Sequence 8135, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 8135
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-8135
Query Match 37.5%; Score 6; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SLPKSE 7
Db 165 SLPKSE 170
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RESULT 11
US-09-107-433-4311
; Sequence 4311, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4311:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 284 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...284
; SEQUENCE DESCRIPTION: SEQ ID NO: 4311:
US-09-107-433-4311
Query Match 37.5%; Score 6; DB 4; Length 284;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 KSEFAV 10
Db 74 KSEFAV 79
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RESULT 12
US-09-902-540-13383
; Sequence 13383, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13383
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13383
Query Match 37.5%; Score 6; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 PDLELP 16
Db 55 PDLELP 60
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RESULT 13
US-09-719-108-6
; Sequence 6, Application US/09719108
; Patent No. 6670527
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/09/719,108
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6

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; LENGTH: 329
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-719-108-6

Query Match      37.5%; Score 6; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SLPKSE 7
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Db      66 SLPKSE 71

RESULT 14
US-09-270-767-42023
; Sequence 42023, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42023
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-42023

Query Match      37.5%; Score 6; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 PDLELP 16
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Db      200 PDLELP 205

RESULT 15
US-09-270-767-46804
; Sequence 46804, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46804
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-46804

Query Match      37.5%; Score 6; DB 4; Length 356;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SLPKSE 7
      |||||
Db      333 SLPKSE 338
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Title: US-10-030-937-72
Perfect score: 16
Sequence: 1 YSLPKSEFAVPDLPLP 16

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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	50.0	193	15	US-10-170-385-389 Sequence 389, App
2	8	50.0	193	16	US-10-723-860-529 Sequence 529, App
3	7	43.8	54	16	US-10-425-115-220040 Sequence 220040, App
4	6	37.5	39	11	US-09-833-245-1222 Sequence 1222, App
5	6	37.5	39	11	US-09-833-245-1224 Sequence 1224, App
6	6	37.5	51	16	US-10-437-963-105909 Sequence 105909, App
7	6	37.5	71	16	US-10-425-115-252984 Sequence 252984, App
8	6	37.5	86	16	US-10-437-963-188997 Sequence 188997, App
9	6	37.5	92	15	US-10-424-599-247004 Sequence 247004, App
10	6	37.5	95	9	US-09-925-299-1494 Sequence 1494, App
11	6	37.5	95	10	US-09-925-299-1494 Sequence 1494, App

12	6	37.5	101	15	US-10-282-122A-46052	Sequence 46052, A
13	6	37.5	116	15	US-10-424-599-188964	Sequence 188964, A
14	6	37.5	117	16	US-10-425-115-358214	Sequence 358214, A
15	6	37.5	120	15	US-10-424-599-284187	Sequence 284187, A
16	6	37.5	127	16	US-10-437-963-190106	Sequence 190106, A
17	6	37.5	129	16	US-10-437-963-133889	Sequence 133889, A
18	6	37.5	131	15	US-10-425-114-57104	Sequence 57104, A
19	6	37.5	151	9	US-09-738-626-4847	Sequence 4847, App
20	6	37.5	157	16	US-10-425-115-269204	Sequence 269204, A
21	6	37.5	158	17	US-10-732-923-21187	Sequence 21187, A
22	6	37.5	165	15	US-10-425-114-64412	Sequence 64412, A
23	6	37.5	176	14	US-10-168-066-6	Sequence 6, Appli
24	6	37.5	176	16	US-10-408-765A-1852	Sequence 1852, App
25	6	37.5	202	16	US-10-767-701-54502	Sequence 54502, A
26	6	37.5	214	9	US-09-999-602-1	Sequence 1, Appli
27	6	37.5	214	15	US-10-282-122A-69056	Sequence 69056, A
28	6	37.5	216	14	US-10-301-822-217	Sequence 217, App
29	6	37.5	216	15	US-10-425-114-50218	Sequence 50218, A
30	6	37.5	216	16	US-10-734-564-111	Sequence 111, App
31	6	37.5	220	17	US-10-732-923-21147	Sequence 21147, A
32	6	37.5	220	17	US-10-732-923-21391	Sequence 21391, A
33	6	37.5	227	16	US-10-425-115-255964	Sequence 255964, A
34	6	37.5	249	15	US-10-425-114-69119	Sequence 69119, A
35	6	37.5	251	14	US-10-301-822-220	Sequence 220, App
36	6	37.5	255	15	US-10-457-372-11	GENERAL INFORMA
37	6	37.5	257	14	US-10-106-698-6128	Sequence 6128, Ap
38	6	37.5	257	15	US-10-457-372-13	GENERAL INFORMA
39	6	37.5	267	14	US-10-301-822-215	Sequence 215, App
40	6	37.5	284	18	US-10-617-320-4311	Sequence 4311, App
41	6	37.5	295	15	US-10-425-114-37694	Sequence 37694, A
42	6	37.5	319	15	US-10-282-122A-50380	Sequence 50380, A
43	6	37.5	329	16	US-10-670-454-6	Sequence 6, Appli
44	6	37.5	330	15	US-10-155-435-10	Sequence 10, Appl
45	6	37.5	347	15	US-10-424-599-162707	Sequence 162707, A

ALIGNMENTS

RESULT 1
US-10-170-385-389
; Sequence 389, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-385-389

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Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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QY      1 YSLPKSEF 8
Db      145 YSLPKSEF 152

RESULT 2
US-10-723-860-529
; Sequence 529, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 529
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-529

Query Match      50.0%; Score 8; DB 16; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSLPKSEF 8
Db      145 YSLPKSEF 152

RESULT 3
US-10-425-115-220040
; Sequence 220040, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 220040
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(54)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_132263C.1.pep
US-10-425-115-220040

Query Match      43.8%; Score 7; DB 16; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 AVPDLEL 15
Db     10 AVPDLEL 16

Query Match      37.5%; Score 6; DB 11; Length 39;
Best Local Similarity 100.0%; Pred. No. 42;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-09-833-245-1222
; Sequence 1222, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1222
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-1222

Query Match      37.5%; Score 6; DB 11; Length 39;
Best Local Similarity 100.0%; Pred. No. 42;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 VPDLEL 15
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RESULT 5
US-09-833-245-1224
; Sequence 1224, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1224
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-1224

Query Match      37.5%; Score 6; DB 11; Length 39;
Best Local Similarity 100.0%; Pred. No. 42;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 VPDLEL 15
Db       4 VPDLEL 9

RESULT 6
US-10-437-963-105909
; Sequence 105909, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
```

```
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 105909
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_10402C.1.pep
US-10-437-963-105909

Query Match      37.5%; Score 6; DB 16; Length 51;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSLPKS 6
Db      10 YSLPKS 15

RESULT 7
US-10-425-115-252984
; Sequence 252984, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 252984
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_162304C.1.pep
US-10-425-115-252984

Query Match      37.5%; Score 6; DB 16; Length 71;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 VPDLEL 15
Db      14 VPDLEL 19

RESULT 8
US-10-437-963-188997
; Sequence 188997, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
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; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 188997
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_85548C.1.pep
US-10-437-963-188997

Query Match      37.5%; Score 6; DB 16; Length 86;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 FAVPDL 13
Db      45 FAVPDL 50

RESULT 9
US-10-424-599-247004
; Sequence 247004, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 247004
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65074C.1.pep
US-10-424-599-247004

Query Match      37.5%; Score 6; DB 15; Length 92;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 PDLELP 16
Db      43 PDLELP 48

RESULT 10
US-09-925-299-1494
; Sequence 1494, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 1494
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (91)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (94)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (95)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1494

Query Match 37.5%; Score 6; DB 9; Length 95;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PDLELP 16
Db 54 PDLELP 59

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; Sequence 1494, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1494
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (91)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (94)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (95)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1494

Query Match 37.5%; Score 6; DB 10; Length 95;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PDLELP 16
Db 54 PDLELP 59

RESULT 12

US-10-282-122A-46052
; Sequence 46052, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46052
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-282-122A-46052

Query Match 37.5%; Score 6; DB 15; Length 101;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SLPKSE 7
Db 13 SLPKSE 18

RESULT 13
US-10-424-599-188964
; Sequence 188964, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684

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; SEQ ID NO 188964
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_141649C.1.pep
US-10-424-599-188964

Query Match      37.5%; Score 6; DB 15; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 KSEFAV 10
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Db      86 KSEFAV 91

RESULT 14
US-10-425-115-358214
; Sequence 358214, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 358214
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(117)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_89859C.1.pep
US-10-425-115-358214

Query Match      37.5%; Score 6; DB 16; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 PDLELP 16
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Db      18 PDLELP 23

RESULT 15
US-10-424-599-284187
; Sequence 284187, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 284187
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_98646C.1.pep
US-10-424-599-284187

Query Match      37.5%; Score 6; DB 15; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 PDLELP 16
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Db      107 PDLELP 112

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Title: US-10-030-937-72
Perfect score: 83
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10030937/runat_26072005_132236_10399/app_query.fasta_1.789
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10030937@cgn1_1_116@runat_26072005_132236_10399 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	56.6	8220	2 US-08-568-459A-11	Sequence 11, Appl
2	47	56.6	8220	2 US-08-487-826B-11	Sequence 11, Appl
3	47	56.6	8220	3 US-09-210-288-11	Sequence 11, Appl
4	47	56.6	9280	4 US-08-956-171E-131	Sequence 131, App
5	47	56.6	9280	4 US-08-781-986A-131	Sequence 131, App
6	47	56.6	19124	2 US-08-487-826B-13	Sequence 13, Appl
c 7	47	56.6	450395	4 US-09-949-016-15473	Sequence 15473, A
c 8	46	55.4	1062	4 US-09-894-844-61	Sequence 61, Appl
9	46	55.4	4403765	3 US-09-103-840A-2	Sequence 2, Appli
c 10	46	55.4	4403765	3 US-09-103-840A-2	Sequence 2, Appli
11	46	55.4	4411529	3 US-09-103-840A-1	Sequence 1, Appli
c 12	46	55.4	4411529	3 US-09-103-840A-1	Sequence 1, Appli

13	44	53.0	924	4 US-09-543-681A-69	Sequence 69, Appl
14	44	53.0	17154	4 US-09-949-016-16889	Sequence 16889, A
c 15	44	53.0	31407	4 US-09-949-016-17359	Sequence 17359, A
c 16	44	53.0	46343	4 US-09-949-016-16824	Sequence 16824, A
17	44	53.0	64291	4 US-09-949-016-16278	Sequence 16278, A
18	44	53.0	117410	4 US-09-949-016-12262	Sequence 12262, A
c 19	43	51.8	601	4 US-09-949-016-20153	Sequence 20153, A
c 20	43	51.8	601	4 US-09-949-016-119374	Sequence 119374, A
21	43	51.8	1416	3 US-08-911-853-3	Sequence 3, Appli
22	43	51.8	1416	3 US-09-479-409-3	Sequence 3, Appli
23	43	51.8	1416	3 US-09-479-453-3	Sequence 3, Appli
24	43	51.8	2439	4 US-09-489-039A-7111	Sequence 7111, Ap
25	43	51.8	4377	3 US-08-911-853-28	Sequence 28, Appl
26	43	51.8	4377	3 US-09-479-409-28	Sequence 28, Appl
27	43	51.8	4377	3 US-09-479-453-28	Sequence 28, Appl
28	43	51.8	6308	4 US-09-949-016-12496	Sequence 12496, A
29	43	51.8	7144	4 US-09-949-016-14392	Sequence 14392, A
c 30	43	51.8	10086	4 US-09-949-016-15056	Sequence 15056, A
c 31	43	51.8	35064	4 US-09-949-016-12778	Sequence 12778, A
c 32	43	51.8	35065	4 US-09-949-016-13196	Sequence 13196, A
c 33	43	51.8	112132	3 US-09-741-150-3	Sequence 3, Appli
c 34	43	51.8	112132	4 US-10-160-187-3	Sequence 3, Appli
35	43	51.8	1830121	4 US-09-557-884-1	Sequence 1, Appli
36	43	51.8	1830121	4 US-09-643-990A-1	Sequence 1, Appli
37	42	50.6	354	4 US-09-513-999C-13536	Sequence 13536, A
c 38	42	50.6	601	4 US-09-949-016-87635	Sequence 87635, A
c 39	42	50.6	601	4 US-09-949-016-87636	Sequence 87636, A
c 40	42	50.6	601	4 US-09-949-016-87637	Sequence 87637, A
41	42	50.6	601	4 US-09-949-016-91953	Sequence 91953, A
42	42	50.6	601	4 US-09-949-016-91954	Sequence 91954, A
43	42	50.6	601	4 US-09-949-016-91955	Sequence 91955, A
44	42	50.6	1256	4 US-09-902-540-5454	Sequence 5454, Ap
45	42	50.6	1404	4 US-09-614-221A-277	Sequence 277, App

ALIGNMENTS

RESULT 1

US-08-568-459A-11
; Sequence 11, Application US/08568459A
; Patent No. 5849306

GENERAL INFORMATION:

; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellem, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660

Result No.

Score Query Match Length DB ID Description

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; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 8220 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   HYPOTHETICAL: NO
;   ORIGINAL SOURCE:
;     ORGANISM: Plasmodium falciparum
;     US-08-568-459A-11

Alignment Scores:      228      Length: 8220
Pred. No.:            47.00    Matches: 9
Score:                78.57%   Conservative: 2
Percent Similarity:    64.29%   Mismatches: 3
Best Local Similarity: 56.63%   Indels: 0
Query Match:          2       Gaps: 0
DB:

US-10-030-937-72 (1-16) x US-08-568-459A-11 (1-8220)

Qy      3 LeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db      6341 CTTCCAAAAACGATGGAACGTGTTCCGGATTAGAAAAGCCG 6382

RESULT 2
US-08-487-826B-11
; Sequence 11, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
;   APPLICANT: Sim, Kim L.
;   APPLICANT: Chitnis, Chetan
;   APPLICANT: Miller, Louis H.
;   APPLICANT: Peterson, David S.
;   APPLICANT: Su, Xin-zhaun
;   APPLICANT: Wellem, Thomas E.
;   TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
;   TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Knobbe Martens Olson & Bear
;     STREET: 620 Newport Center Drive 16th Floor
;     CITY: Newport Beach
;     STATE: California
;     COUNTRY: US
;     ZIP: 92660
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/487,826B
;     FILING DATE: 10-SEP-1993
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Israelsen, Ned
;     REGISTRATION NUMBER: 29,655
;     REFERENCE/DOCKET NUMBER: NIH121.001CP1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (619) 235-8550
;     TELEFAX: (619) 235-0176
;   INFORMATION FOR SEQ ID NO: 11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 8220 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ORIGINAL SOURCE:
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; ORGANISM: Plasmodium falciparum
; US-08-487-826B-11

Alignment Scores:      228      Length: 8220
Pred. No.:            47.00    Matches: 9
Score:                78.57%   Conservative: 2
Percent Similarity:    64.29%   Mismatches: 3
Best Local Similarity: 56.63%   Indels: 0
Query Match:          2       Gaps: 0
DB:

US-10-030-937-72 (1-16) x US-08-487-826B-11 (1-8220)

Qy      3 LeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db      6341 CTTCCAAAAACGATGGAACGTGTTCCGGATTAGAAAAGCCG 6382

RESULT 3
US-09-210-288-11
; Sequence 11, Application US/09210288
; Patent No. 6392026
; GENERAL INFORMATION:
;   APPLICANT: Sim, Kim L.
;   APPLICANT: Chitnis, Chetan
;   APPLICANT: Miller, Louis H.
;   APPLICANT: Peterson, David S.
;   APPLICANT: Su, Xin-zhaun
;   APPLICANT: Wellem, Thomas E.
;   TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
;   TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
;   NUMBER OF SEQUENCES: 37
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Knobbe Martens Olson & Bear
;     STREET: 620 Newport Center Drive 16th Floor
;     CITY: Newport Beach
;     STATE: California
;     COUNTRY: US
;     ZIP: 92660
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/210,288
;     FILING DATE:
;     CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Fuller, Michael
;     REGISTRATION NUMBER: 36,516
;     REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (619) 235-8550
;     TELEFAX: (619) 235-0176
;   INFORMATION FOR SEQ ID NO: 11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 8220 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ORIGINAL SOURCE:
;     ORGANISM: Plasmodium falciparum
;     US-09-210-288-11

Alignment Scores:      228      Length: 8220
Pred. No.:            47.00    Matches: 9
Score:                78.57%   Conservative: 2
Percent Similarity:    64.29%   Mismatches: 3
Best Local Similarity: 56.63%   Indels: 0
Query Match:          3       Gaps: 0
DB:
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US-10-030-937-72 (1-16) x US-09-210-288-11 (1-8220)

Qy 3 LeuProLySerGluPheAlaValProAspLeuGluLeuPro 16
Db 6341 CTTCCAAAAACGATCGAAGTTGTCGGATTAGAAAACCG 6382

RESULT 4

US-08-956-171E-131
; Sequence 131, Application US/08956171E
; Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 131:

SEQUENCE CHARACTERISTICS:

LENGTH: 9280 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 131:

US-08-956-171E-131

Alignment Scores:

Pred. No.: 265 Length: 9280
Score: 47.00 Matches: 8
Percent Similarity: 86.67% Conservative: 5
Best Local Similarity: 53.33% Mismatches: 2
Query Match: 56.63% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-72 (1-16) x US-08-956-171E-131 (1-9280)

Qy 2 SerLeuProLySerGluPheAlaValProAspLeuGluLeuPro 16

Db 6399 ACGTTCGGAATCAAAGTTGCTTTACCACCAATATTCATACCA 6443

RESULT 5

US-08-781-986A-131

; Sequence 131, Application US/08781986A

; Patent No. 6737248

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 131:

SEQUENCE CHARACTERISTICS:

LENGTH: 9280 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-781-986A-131

Alignment Scores:

Pred. No.: 265 Length: 9280
Score: 47.00 Matches: 8
Percent Similarity: 86.67% Conservative: 5
Best Local Similarity: 53.33% Mismatches: 2
Query Match: 56.63% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-72 (1-16) x US-08-781-986A-131 (1-9280)

Qy 2 SerLeuProLySerGluPheAlaValProAspLeuGluLeuPro 16

Db 6399 ACGTTCGGAATCAAAGTTGCTTTACCACCAATATTCATACCA 6443

RESULT 6

US-08-487-826B-13

; Sequence 13, Application US/08487826B

; Patent No. 5993827

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.

APPLICANT: Chitnis, Chetan

APPLICANT: Miller, Louis H.

APPLICANT: Peterson, David S.

APPLICANT: Su, Xin-zhaun

APPLICANT: Wellem, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX

TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe Martens Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: California

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; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-487-826B-13

Alignment Scores:
Pred. No.: 660 Length: 19124
Score: 47.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 56.63% Indels: 0
DB: 2 Gaps: 0

US-10-030-937-72 (1-16) x US-08-487-826B-13 (1-19124)

Qy 3 LeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 13661 CTTCCAAAACGATGGAAGTCTCCGGATTAGAAAAGCCG 13702

RESULT 7
US-09-949-016-15473/c
; Sequence 15473, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15473
; LENGTH: 450395
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(450395)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15473
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Alignment Scores:

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; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-487-826B-13

Alignment Scores:
Pred. No.: 660 Length: 19124
Score: 47.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 56.63% Indels: 0
DB: 2 Gaps: 0

US-10-030-937-72 (1-16) x US-08-487-826B-13 (1-19124)

Qy 3 LeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 13661 CTTCCAAAACGATGGAAGTCTCCGGATTAGAAAAGCCG 13702

RESULT 7
US-09-949-016-15473/c
; Sequence 15473, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15473
; LENGTH: 450395
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(450395)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15473

Pred. No.: 3.53e+04 Length: 450395
Score: 47.00 Matches: 8
Percent Similarity: 84.62% Conservative: 3
Best Local Similarity: 61.54% Mismatches: 2
Query Match: 56.63% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-72 (1-16) x US-09-949-016-15473 (1-450395)

Qy 1 TyrSerLeuProLysSerGluPheAlaValProAspLeu 13
Db 110299 TATAGCATGCCCAAACTGAGTTCCCTGCTCCCTCCCTC 110261

RESULT 8
US-09-894-844-61/c
; Sequence 61, Application US/09894844
; Patent No. 6686166
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894,844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-09-894-844-61

Alignment Scores:
Pred. No.: 26.7 Length: 1062
Score: 46.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 55.42% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-72 (1-16) x US-09-894-844-61 (1-1062)

Qy 3 LeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 839 TTGCCGAAGCCCGAGTTCTGATGATGCCCGAGTTGCCACTGCCA 798

RESULT 9
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
```

; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.: 8.05e+05 Length: 4403765
Score: 46.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 55.42% Indels: 0
DB: 3 Gaps: 0

US-10-030-937-72 (1-16) x US-09-103-840A-2 (1-4403765)
Qy 3 LeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 2632604 TTGCCGAAGCCCGAGTTCTGTAATGCCCGAGTTGCCACTGCCA 2632645

RESULT 10
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.: 8.05e+05 Length: 4403765
Score: 46.00 Matches: 8
Percent Similarity: 68.75% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 55.42% Indels: 0
DB: 3 Gaps: 0

US-10-030-937-72 (1-16) x US-09-103-840A-2 (1-4403765)
Qy 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 299240 TACAGCGCACCGAAGCCGAGGCGGCCACACCCGAGACGACCATCCCG 299193

RESULT 11
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 8.06e+05 Length: 4411529
Score: 46.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 55.42% Indels: 0
DB: 3 Gaps: 0

US-10-030-937-72 (1-16) x US-09-103-840A-1 (1-4411529)
Qy 3 LeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 2634752 TTGCCGAAGCCCGAGTTCTGTAATGCCCGAGTTGCCACTGCCA 2634793

RESULT 12
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 8.06e+05 Length: 4411529
Score: 46.00 Matches: 8
Percent Similarity: 68.75% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 55.42% Indels: 0
DB: 3 Gaps: 0

US-10-030-937-72 (1-16) x US-09-103-840A-1 (1-4411529)
Qy 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 299129 TACAGCGCACCGAAGCCGAGGCGGCCACACCCGAGACGACCATCCCG 299082

RESULT 13
US-09-543-681A-69
; Sequence 69, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706

; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 69
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-69

Alignment Scores:
Pred. No.: 53.8 Length: 924
Score: 44.00 Matches: 7
Percent Similarity: 78.57% Conservative: 4
Best Local Similarity: 50.00% Mismatches: 3
Query Match: 53.01% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-72 (1-16) x US-09-543-681A-69 (1-924)

Qy 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGlu 14
|||||::: |||||:::
Db 658 TACAGTTTACTCAACCAATTACTGATCTGATATTCAA 699

RESULT 14

US-09-949-016-16889
; Sequence 16889, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16889
; LENGTH: 17154
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16889

Alignment Scores:
Pred. No.: 2.15e+03 Length: 17154
Score: 44.00 Matches: 9
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 53.01% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-72 (1-16) x US-09-949-016-16889 (1-17154)

Qy 2 SerLeuProLysSerGluPheAlaValProAspLeu 13
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Db 13244 TCCCTGCCAAATCGGCTTTGCCCTTCCCACTCTG 13279

RESULT 15

US-09-949-016-17359/c
; Sequence 17359, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17359
; LENGTH: 31407
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(31407)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17359

Alignment Scores:

Pred. No.: 4.6e+03 Length: 31407
Score: 44.00 Matches: 8
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 53.01% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-72 (1-16) x US-09-949-016-17359 (1-31407)

Qy 7 GluPheAlaValProAspLeuGluLeu 15
|||||::: |||||:::
Db 2930 GAATTTGCCATCCCTGATTAGAACTT 2904

Search completed: July 27, 2005, 19:54:20
Job time : 860.453 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 27, 2005, 19:25:25 ; Search time 98.6311 Seconds
(without alignments)
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Title: US-10-030-937-72
Perfect score: 83
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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7277826 seqs, 3233139505 residues

Total number of hits satisfying chosen parameters: 14555652

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	95.2	448	11	US-09-969-034-4215 Sequence 4215, Ap
2	79	95.2	953	20	US-10-723-860-528 Sequence 528, App
3	79	95.2	1935	10	US-09-971-392-102 Sequence 102, App
4	79	95.2	2384	9	US-09-822-849A-53 Sequence 53, Appl
5	79	95.2	2436	9	US-09-954-531-380 Sequence 380, App
6	79	95.2	2436	10	US-09-525-978B-81 Sequence 81, Appl
7	79	95.2	2436	21	US-10-843-641A-1447 Sequence 1447, Ap
8	79	95.2	2478	17	US-10-170-385-390 Sequence 390, App
9	79	95.2	3988	20	US-10-723-860-5187 Sequence 5187, Ap
c 10	79	95.2	250000	16	US-10-225-810-26 Sequence 26, Appl
11	69	83.1	1983	17	US-10-388-934-167 Sequence 167, App
12	68	81.9	596	22	US-10-972-079-7219 Sequence 7219, Ap
13	68	81.9	599	22	US-10-972-079-7218 Sequence 7218, Ap
14	49	59.0	2269	19	US-10-437-963-4335 Sequence 4335, Ap
c 15	48	57.8	475	19	US-10-021-323-4461 Sequence 4461, Ap
16	48	57.8	475	19	US-10-767-795-2700 Sequence 2700, Ap
c 17	48	57.8	2796	19	US-10-437-963-97626 Sequence 97626, A
c 18	48	57.8	3335	19	US-10-437-963-97629 Sequence 97629, A
c 19	47	56.6	790	20	US-10-653-047-4552 Sequence 4552, Ap
c 20	47	56.6	3700	21	US-10-899-942-6 Sequence 6, Appli
21	47	56.6	8220	13	US-10-153-273-11 Sequence 11, Appl
22	47	56.6	9280	8	US-08-781-986A-131 Sequence 131, App
23	47	56.6	9280	18	US-10-329-624-131 Sequence 31, Appl
c 24	47	56.6	68233	17	US-10-034-650-31 Sequence 1726, Ap
c 25	47	56.6	122614	13	US-10-087-192-1726 Sequence 5, Appli
c 26	47	56.6	402850	10	US-09-844-653-5 Sequence 45305, A
c 27	46	55.4	442	20	US-10-425-115-45305 Sequence 246658,
28	46	55.4	535	13	US-10-027-632-246658 Sequence 246658,
29	46	55.4	535	17	US-10-027-632-246658 Sequence 61, Appl
c 30	46	55.4	1062	9	US-09-894-844-61 Sequence 61, Appl
c 31	46	55.4	1062	17	US-10-388-902-61 Sequence 61, Appl
c 32	46	55.4	1062	18	US-10-647-089-61 Sequence 50, Appl
33	46	55.4	4999	15	US-10-225-486-50 Sequence 3784, Ap
34	46	55.4	4999	20	US-10-723-860-3784 Sequence 57, Appl
35	46	55.4	4999	21	US-10-651-237-57 Sequence 57, Appl
36	46	55.4	4999	21	US-10-782-413-57 Sequence 7718, Ap
37	46	55.4	5755	20	US-10-723-860-4061 Sequence 4061, Ap
38	45	54.2	350	20	US-10-357-930-53483 Sequence 53483, A
c 39	45	54.2	626	20	US-10-282-122A-24975 Sequence 24975, A
c 40	45	54.2	1200	17	US-10-172-118-1397 Sequence 1397, Ap
41	45	54.2	1749	17	US-10-295-027-457 Sequence 457, App
42	45	54.2	1749	17	US-10-295-027-1095 Sequence 1095, Ap
43	45	54.2	1749	17	US-10-342-887-1397 Sequence 1397, Ap
44	45	54.2	1749	18	US-10-342-887-1397 Sequence 34, Appl
45	45	54.2	1749	20	US-10-422-522-34

ALIGNMENTS

RESULT 1
US-09-969-034-4215
; Sequence 4215, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poornima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; TITLE OF INVENTION: Expressed in Cancer Tissue
; FILE REFERENCE: 1657/1032

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; CURRENT APPLICATION NUMBER: US/09/969,034
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4215
; LENGTH: 448
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 241, 277, 288, 295, 299, 300, 304, 310, 316, 343, 346, 356,
; LOCATION: 364, 370, 396, 397, 406, 410, 415, 424, 437
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-4215

Alignment Scores:
Pred. No.:      2.68e-05      Length:      448
Score:          79.00        Matches:      15
Percent Similarity: 93.75%    Conservative: 0
Best Local Similarity: 93.75% Mismatches:      1
Query Match:    95.18%      Indels:        0
DB:             11          Gaps:          0

US-10-030-937-72 (1-16) x US-09-969-034-4215 (1-448)

Qy      1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db      43 TACTCACTGCCCCAAGAGCGAATTGTTGTGCTGACCTGGAGCTGCC 90

RESULT 2
US-10-723-860-528
; Sequence 528, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 528
; LENGTH: 953
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-528

Alignment Scores:
Pred. No.:      6.36e-05      Length:      953
Score:          79.00        Matches:      15
Percent Similarity: 93.75%    Conservative: 0
Best Local Similarity: 93.75% Mismatches:      1
Query Match:    95.18%      Indels:        0
DB:             20          Gaps:          0

US-10-030-937-72 (1-16) x US-10-723-860-528 (1-953)

Qy      1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db      523 TACTCACTGCCCCAAGAGCGAATTGTTGTGCTGACCTGGAGCTGCC 570

RESULT 3
US-09-971-392-102
; Sequence 102, Application US/09971392
; Publication No. US20030134283A1
; GENERAL INFORMATION:
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; APPLICANT: Peterson, David P.
; APPLICANT: Pearson, Cecelia I.
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION
; FILE REFERENCE: PA-0029 US
; CURRENT APPLICATION NUMBER: US/09/971,392
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/237,652
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PERL Program
; SEQ ID NO 102
; LENGTH: 1935
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Template ID: 977615.8
US-09-971-392-102

Alignment Scores:
Pred. No.:      0.000143      Length:      1935
Score:          79.00        Matches:      15
Percent Similarity: 93.75%    Conservative: 0
Best Local Similarity: 93.75% Mismatches:      1
Query Match:    95.18%      Indels:        0
DB:             10          Gaps:          0

US-10-030-937-72 (1-16) x US-09-971-392-102 (1-1935)

Qy      1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db      534 TACTCACTGCCCCAAGAGCGAATTGTTGTGCTGACCTGGAGCTGCC 581

RESULT 4
US-09-822-849A-53
; Sequence 53, Application US/09822849A
; Patent No. US20020045170A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6403
; CURRENT APPLICATION NUMBER: US/09/822,849A
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/195,582
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 598
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 2384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-849A-53

Alignment Scores:
Pred. No.:      0.000182      Length:      2384
Score:          79.00        Matches:      15
Percent Similarity: 93.75%    Conservative: 0
Best Local Similarity: 93.75% Mismatches:      1
Query Match:    95.18%      Indels:        0
DB:             9          Gaps:          0

US-10-030-937-72 (1-16) x US-09-822-849A-53 (1-2384)

Qy      1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
```


Db 445 TACTCACTGCCCAAGAGCGAATTCGTTGTGCTGCTGACTGGAGCTGCC 492

RESULT 5

US-09-954-531-380
; Sequence 380, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 380
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-380

Alignment Scores:
Pred. No.: 0.000187 Length: 2436
Score: 79.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 95.18% Indels: 0
DB: 9 Gaps: 0

US-10-030-937-72 (1-16) x US-09-954-531-380 (1-2436)

QY 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 491 TACTCACTGCCCAAGAGCGAATTCGTTGTGCTGCTGACTGGAGCTGCC 538

RESULT 6

US-09-525-978B-81
; Sequence 81, Application US/09525978B
; Publication No. US2003004972A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Caras, Ingrid W.
; APPLICANT: Hevezi, Peter
; APPLICANT: Wilson, Keith
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING MACROPHAGE DEVELOPMENT
; TITLE OF INVENTION: RELATED DISORDERS, COMPOSITIONS, AND METHODS OF
; TITLE OF INVENTION: SCREENING FOR MACROPHAGE DEVELOPMENT MODULATORS
; FILE REFERENCE: A-67413-1/DJB/JJD
; CURRENT APPLICATION NUMBER: US/09/525,978B
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: USSN 60/124,530
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-525-978B-81

Alignment Scores:
Pred. No.: 0.000187 Length: 2436

Score: 79.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 95.18% Indels: 0
DB: 10 Gaps: 0

US-10-030-937-72 (1-16) x US-09-525-978B-81 (1-2436)

QY 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 491 TACTCACTGCCCAAGAGCGAATTCGTTGTGCTGCTGACTGGAGCTGCC 538

RESULT 7

US-10-843-641A-1447
; Sequence 1447, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1447
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-1447

Alignment Scores:
Pred. No.: 0.000187 Length: 2436
Score: 79.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 95.18% Indels: 0
DB: 21 Gaps: 0

US-10-030-937-72 (1-16) x US-10-843-641A-1447 (1-2436)

QY 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 491 TACTCACTGCCCAAGAGCGAATTCGTTGTGCTGCTGACTGGAGCTGCC 538

RESULT 8

US-10-170-385-390
; Sequence 390, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert

; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 390
; LENGTH: 2478
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-170-385-390

Alignment Scores:
Pred. No.: 0.00019 Length: 2478
Score: 79.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 95.18% Indels: 0
DB: 17 Gaps: 0

US-10-030-937-72 (1-16) x US-10-170-385-390 (1-2478)

Qy 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 528 TACTCACTGCCCAAGAGCGAATTGTTGTGCCTGACCTGGAGCTGCCC 575

RESULT 9

US-10-723-860-5187
; Sequence 5187, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5187
; LENGTH: 3988
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2864)..(2894)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3472)..(3486)
; OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-5187

Alignment Scores:
Pred. No.: 0.000329 Length: 3988
Score: 79.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0

Best Local Similarity: 93.75% Mismatches: 1
Query Match: 95.18% Indels: 0
DB: 20 Gaps: 0
US-10-030-937-72 (1-16) x US-10-723-860-5187 (1-3988)
Qy 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 528 TACTCACTGCCCAAGAGCGAATTGTTGTGCCTGACCTGGAGCTGCCC 575

RESULT 10

US-10-225-810-26/c
; Sequence 26, Application US/10225810
; Publication No. US20030157512A1
; GENERAL INFORMATION:
; APPLICANT: Bermingham, Jr., John R.
; TITLE OF INVENTION: Tramdorins and Methods of Using Tramdorin
; FILE REFERENCE: McLaugh-07165
; CURRENT APPLICATION NUMBER: US/10/225,810
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 250000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (33774)..(33774)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (42953)..(43052)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (45557)..(45656)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (48203)..(48302)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (49551)..(49650)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51561)..(51660)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (52722)..(52821)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (53864)..(53963)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (55290)..(55389)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (56674)..(56773)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (57879)..(57978)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (78952)..(79051)

OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (85316)..(85415)
OTHER INFORMATION: n is a, c, g, or t
US-10-225-810-26

Alignment Scores:
Pred. No.: 0.0379 Length: 250000
Score: 79.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 95.18% Indels: 0
DB: 16 Gaps: 0

US-10-030-937-72 (1-16) x US-10-225-810-26 (1-250000)

Qy 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 249623 TACTCACTGCCCAAGAGCGAATTCGTGTGCCTGACCTGGAGCTGCCC 249576

RESULT 11
US-10-388-934-167
Sequence 167, Application US/10388934
Publication No. US20040005547A1
GENERAL INFORMATION:
APPLICANT: Boess, Franziska
APPLICANT: Suter-Dick, Laura
APPLICANT: Wolf, Detlef
TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
FILE REFERENCE: 21199
CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 02005336.9
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
SOFTWARE: PatentIn version 3.1
SEQ ID NO 167
LENGTH: 1983
TYPE: DNA
ORGANISM: Rattus sp.
US-10-388-934-167

Alignment Scores:
Pred. No.: 0.0114 Length: 1983
Score: 69.00 Matches: 13
Percent Similarity: 81.25% Conservative: 0
Best Local Similarity: 81.25% Mismatches: 3
Query Match: 83.13% Indels: 0
DB: 17 Gaps: 0

US-10-030-937-72 (1-16) x US-10-388-934-167 (1-1983)
Qy 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 462 TACTCACTGCCTTCGAGCAACTTCACAGTGCCTGATCTGGAGCTTCCA 509

RESULT 12
US-10-972-079-7219
Sequence 7219, Application US/10972079
Publication No. US20050153317A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: ROSENFELD, David
APPLICANT: KERR, Richard
APPLICANT: BATES, Stephen
APPLICANT: HOLM, Tom
TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
FILE REFERENCE: MM1110-2

OTHER INFORMATION: US/10/972,079
CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 60/514,333
PRIOR FILING DATE: 2003-10-24
NUMBER OF SEQ ID NOS: 96631
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7219
LENGTH: 596
TYPE: DNA
ORGANISM: Chicken 19866894191999_2
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(32)
OTHER INFORMATION: n is any nucleotide
US-10-972-079-7219

Alignment Scores:
Pred. No.: 0.00442 Length: 596
Score: 68.00 Matches: 12
Percent Similarity: 93.75% Conservative: 3
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 81.93% Indels: 0
DB: 22 Gaps: 0

US-10-030-937-72 (1-16) x US-10-972-079-7219 (1-596)

Qy 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 353 TACTCACTGCCCGCAGCGACTTCGCCCTGCCGACGTCGAGCTGCC 400

RESULT 13
US-10-972-079-7218
Sequence 7218, Application US/10972079
Publication No. US20050153317A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: ROSENFELD, David
APPLICANT: KERR, Richard
APPLICANT: BATES, Stephen
APPLICANT: HOLM, Tom
TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
FILE REFERENCE: MM1110-2
CURRENT APPLICATION NUMBER: US/10/972,079
CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 60/514,333
PRIOR FILING DATE: 2003-10-24
NUMBER OF SEQ ID NOS: 96631
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7218
LENGTH: 599
TYPE: DNA
ORGANISM: Chicken 19866894191999_1
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(114)
OTHER INFORMATION: n is any nucleotide
US-10-972-079-7218

Alignment Scores:
Pred. No.: 0.00445 Length: 599
Score: 68.00 Matches: 12
Percent Similarity: 93.75% Conservative: 3
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 81.93% Indels: 0
DB: 22 Gaps: 0

US-10-030-937-72 (1-16) x US-10-972-079-7218 (1-599)

Qy 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 435 TACTCACTGCCCGCAGCGACTTCGCCCTGCCGACGTCGAGCTGCC 482

RESULT 14
US-10-437-963-4335
; Sequence 4335, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 4335
; LENGTH: 2269
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(2269)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_11228C.1
US-10-437-963-4335

Alignment Scores:
Pred. No.: 78.9 Length: 2269
Score: 49.00 Matches: 8
Percent Similarity: 92.31% Conservative: 4
Best Local Similarity: 61.54% Mismatches: 1
Query Match: 59.04% Indels: 0
DB: 19 Gaps: 0

US-10-030-937-72 (1-16) x US-10-437-963-4335 (1-2269)

Qy 3 LeuProLysSerGluPheAlaValProAspLeuGluLeu 15
:::||||| ::::|||||
Db 221 GTTCCACGAGTGAATTTCCATACCTGATTGGAGCTT 259

RESULT 15
US-10-021-323-4461/c
; Sequence 4461, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 4461
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3825-025-Q6-N6-C6
US-10-021-323-4461

Alignment Scores:
Pred. No.: 20.3 Length: 475

Score: 48.00 Matches: 10
Percent Similarity: 73.33% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 4
Query Match: 57.83% Indels: 0
DB: 19 Gaps: 0

US-10-030-937-72 (1-16) x US-10-021-323-4461 (1-475)

Qy 2 SerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
||||| ::::|||||
Db 435 TCCCTCCCCAAGGGAACGATGCTGTCCCATTCCTGGAACCTACCA 391

Search completed: July 27, 2005, 22:48:10
Job time : 106.631 secs

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OM protein - protein search, using sw model

Run on: July 27, 2005, 12:32:19 ; Search time 37.7422 Seconds
(without alignments)
381.728 Million cell updates/sec

Title: US-10-030-937-9
Perfect score: 1018
Sequence: 1 MQSLMQAPLLIALGLLATP.....LSSSGKRLGCIKIAASLKGI 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1005	98.7	193	4 US-09-183-841-1	Sequence 1, Appli
2	857	84.2	178	4 US-09-183-841-2	Sequence 2, Appli
3	88.5	8.7	310	4 US-09-976-594-807	Sequence 807, App
4	86.5	8.5	410	3 US-08-630-172-17	Sequence 17, Appl
5	86.5	8.5	410	3 US-09-375-419-17	Sequence 17, Appl
6	86.5	8.5	768	3 US-09-302-812-8	Sequence 8, Appli
7	86.5	8.5	768	3 US-09-511-477-8	Sequence 8, Appli
8	86.5	8.5	768	3 US-09-511-507-8	Sequence 8, Appli
9	86	8.4	143	4 US-09-860-793-3	Sequence 3, Appli
10	83	8.2	572	6 5256770-7	Patent No. 5256770
11	83	8.2	572	6 5256770-7	Patent No. 5256770
12	82	8.1	446	1 US-08-307-444A-5	Sequence 5, Appli
13	82	8.1	446	1 US-08-587-389-5	Sequence 5, Appli
14	82	8.1	456	1 US-08-307-444A-3	Sequence 3, Appli
15	82	8.1	456	1 US-08-307-444A-4	Sequence 4, Appli
16	82	8.1	456	1 US-08-587-389-3	Sequence 3, Appli
17	82	8.1	456	1 US-08-587-389-4	Sequence 4, Appli
18	82	8.1	475	1 US-08-307-444A-1	Sequence 1, Appli
19	82	8.1	475	1 US-08-307-444A-2	Sequence 2, Appli
20	82	8.1	475	1 US-08-587-389-1	Sequence 1, Appli
21	82	8.1	475	1 US-08-587-389-2	Sequence 2, Appli
22	82	8.1	476	1 US-08-014-723-1	Sequence 1, Appli
23	82	8.1	476	1 US-08-014-723-2	Sequence 2, Appli
24	82	8.1	476	1 US-08-014-723-18	Sequence 18, Appl
25	82	8.1	476	1 US-08-110-011A-1	Sequence 1, Appli
26	82	8.1	476	1 US-08-110-011A-2	Sequence 2, Appli
27	82	8.1	476	1 US-08-110-011A-18	Sequence 18, Appli

28	82	8.1	494	1 US-08-014-723-14	Sequence 14, Appl
29	82	8.1	494	1 US-08-014-723-16	Sequence 16, Appl
30	82	8.1	494	1 US-08-110-011A-14	Sequence 14, Appl
31	82	8.1	494	1 US-08-110-011A-16	Sequence 16, Appl
32	82	8.1	497	1 US-08-312-870-3	Sequence 3, Appli
33	82	8.1	497	4 US-09-331-793-4	Sequence 4, Appli
34	82	8.1	498	2 US-08-733-564-2	Sequence 2, Appli
35	82	8.1	516	4 US-09-509-994-1	Sequence 1, Appli
36	82	8.1	516	4 US-09-509-994-2	Sequence 2, Appli
37	82	8.1	575	1 US-08-261-206A-59	Sequence 59, Appl
38	82	8.1	575	1 US-08-312-870-1	Sequence 1, Appli
39	82	8.1	575	1 US-08-170-290A-54	Sequence 54, Appl
40	82	8.1	575	4 US-09-880-484D-2	Sequence 2, Appli
41	82	8.1	575	4 US-10-438-648-2	Sequence 2, Appli
42	82	8.1	575	6 5466668-6	Patent No. 5466668
43	82	8.1	575	6 5466668-6	Patent No. 5466668
44	82	8.1	746	4 US-09-370-838-185	Sequence 185, App
45	82	8.1	746	4 US-09-854-133-185	Sequence 185, App

ALIGNMENTS

RESULT 1
US-09-183-841-1
; Sequence 1, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: van20010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (33)..(55)
; FEATURE:
; OTHER INFORMATION: residues 56-63 are included in a further precursor
; OTHER INFORMATION: form of the protein
US-09-183-841-1

Query Match	98.7%	Score 1005;	DB 4;	Length 193;
Best Local Similarity	99.0%	Pred. No. 5.5e-110;		
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Qy	1	MQSLMQAPLLIALGLLATPAQAHLKPKSOLFSSFSWDCNCEGKDPAVIRSLTLEPDP	PVV 60	
Db	1	MQSLMQAPLLIALGLLATPAQAHLKPKSOLFSSFSWDCNCEGKDPAVIRSLTLEPDP	PVV 60	
Qy	61	PGNVTLSVVGSTSVPLSSPLKVDLVLEKEVAGLWIKIPCTDIYIGSCTFEHFCVDLMDLIP	120	
Db	61	PGNVTLSVVGSTSVPLSSPLKVDLVLEKEVAGLWIKIPCTDIYIGSCTFEHFCVDLMDLIP	120	
Qy	121	TGEPCEPEPLRTYGLPCHCPKEGTYSLPKSEFAVPDLELPSWLTGTGNRYIESVLSSSGKR	180	
Db	121	TGEPCEPEPLRTYGLPCHCPKEGTYSLPKSEFAVPDLELPSWLTGTGNRYIESVLSSSGKR	180	
Qy	181	LGCIKIAASLKGI	193	
Db	181	LGCIKIAASLKGI	193	

RESULT 2
US-09-183-841-2
; Sequence 2, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, 35th Floor
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/375,419
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,172
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-375-419-17

Query Match 8.5%; Score 86.5; DB 3; Length 410;
Best Local Similarity 25.6%; Pred. No. 0.21;
Matches 42; Conservative 14; Mismatches 43; Indels 65; Gaps 9;
QY 26 KKPQLSSPS-----WDCFCGKDPVIRSLTLEPDIW-----PGNVTLSSVVGST- 72
Db 46 KGPSKLNDRADSRRLWD---QGNFPLIKLKIEDSDTYICEVEDQKEEVQLLVFLTA 102
QY 73 -----SVPLSSP-----LKVLDLVLEKEVAGLWIKIP 98
Db 103 NSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVS-QLELQDAGTWI--- 158
QY 99 CTDYIGSCTFEHFCVDVLDMLIPTG---EPCPEPLRTYGLPCHCP 139
Db 159 CTVLQKQKVEFKIDIVVLAEPRTIKPCP-----PCKCP 194

RESULT 6
US-09-302-812-8
; Sequence 8, Application US/09302812B
; Patent No. 6333148
; GENERAL INFORMATION:
; APPLICANT: JACOBSON, Myron K.
; APPLICANT: JACOBSON, Elaine L.
; APPLICANT: AM, Jean-Christophe
; APPLICANT: LIN, Winston
; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY (ADP-RIBOSE) GLYCOHYDROLASE (PARG) ENZ
; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: NIAD 201
; CURRENT APPLICATION NUMBER: US/09/302,812B
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,768
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 8
; LENGTH: 768
; TYPE: PRT
; ORGANISM: Drosophila melanogaster

; FEATURE:
US-09-302-812-8
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Best Local Similarity 25.4%; Pred. No. 0.52;
Matches 53; Conservative 25; Mismatches 94; Indels 37; Gaps 9;
QY 3 SLMQAPLLIALGLLLATPAQAHKKPSQLSSP---SWDNCFCGKDPVIRSL----- 51
Db 245 SQQIISCLLANAFCTFPRRNTLKRKSEYSTFPDINFNRLYQSTGPAVLEKLCIMHYFR 304
QY 52 ---TLEPDPVVPGNVTLSSVVG-----TSVPLSS-PLKVDL--VLEKEVAGLW 94
Db 305 RVCPTERDASNVPTGVVTFVRRSGLPEHLIDWSQSAAPLGDVPLHVDAGETIEGIGLL 364
QY 95 IKIPCTDYIGSCTFEHFC--DVLDMLIPTGEPCEPL-RTYGLPCHCPFKEGTYSLPKSE 151
Db 365 QVDFANKYLGGLVGHGCVQEEIRFVI-----CPDLLVGKLFTECLRPF-EALVNLGAER 418
QY 152 FAVPDLELPSWLTGTGNYRIESVLSSSGKR 180
Db 419 YSNYTGAGSFEWSGNFEDSTPRDSSGRR 447

RESULT 7
US-09-511-477-8
; Sequence 8, Application US/09511477
; Patent No. 6337202
; GENERAL INFORMATION:
; APPLICANT: JACOBSON, Myron K.
; APPLICANT: JACOBSON, Elaine L.
; APPLICANT: AME, Jean-Christophe
; APPLICANT: LIN, Winston
; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY (ADP-RIBOSE) GLYCOHYDROLASE (PARG) ENZ
; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: NIAD 201
; CURRENT APPLICATION NUMBER: US/09/511,477
; CURRENT FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 09/302,812
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 8
; LENGTH: 768
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
US-09-511-477-8

Query Match 8.5%; Score 86.5; DB 3; Length 768;
Best Local Similarity 25.4%; Pred. No. 0.52;
Matches 53; Conservative 25; Mismatches 94; Indels 37; Gaps 9;
QY 3 SLMQAPLLIALGLLLATPAQAHKKPSQLSSP---SWDNCFCGKDPVIRSL----- 51
Db 245 SQQIISCLLANAFCTFPRRNTLKRKSEYSTFPDINFNRLYQSTGPAVLEKLCIMHYFR 304
QY 52 ---TLEPDPVVPGNVTLSSVVG-----TSVPLSS-PLKVDL--VLEKEVAGLW 94
Db 305 RVCPTERDASNVPTGVVTFVRRSGLPEHLIDWSQSAAPLGDVPLHVDAGETIEGIGLL 364
QY 95 IKIPCTDYIGSCTFEHFC--DVLDMLIPTGEPCEPL-RTYGLPCHCPFKEGTYSLPKSE 151
Db 365 QVDFANKYLGGLVGHGCVQEEIRFVI-----CPDLLVGKLFTECLRPF-EALVNLGAER 418
QY 152 FAVPDLELPSWLTGTGNYRIESVLSSSGKR 180
Db 419 YSNYTGAGSFEWSGNFEDSTPRDSSGRR 447

RESULT 8
US-09-511-507-8
; Sequence 8, Application US/09511507

Db 186 AAVSITYGTPPAARGADFOALPVGSSAA--VAPLGLQLMCTAGNVQGHWAREAPGAW--- 240
Qy 98 PCTDYIGSCTFEHFCVDLMLIPTGEPCEP-----LRTYGLPCHCPFKEGTYSLPKSEPA 153
Db 241 DCSVENGGC--EHACNA-----IPGAPRCQCPAGAALQADGRSCTASATQSCNDLCE-HFC 293
Qy 154 VPDLELPswLTtGNyRIESVLSsSGKRL 181
Db 294 VpNPdQP-----GSY---SCMCETGYRL 313

RESULT 12
US-08-307-444A-5
; Sequence 5, Application US/08307444A
; Patent No. 5516659
; GENERAL INFORMATION:
; APPLICANT: NII, ATSUSHI
; APPLICANT: MORISHITA, HIDEAKI
; APPLICANT: UEMURA, AKIO
; APPLICANT: MOCHIDA, EI
; TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,444A
; FILING DATE: 19-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/835,436
; FILING DATE: 26-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: OLIFF, JAMES A.
; REGISTRATION NUMBER: 27,075
; REFERENCE/DOCKET NUMBER: JAO 27706
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; TELEX: 90-1799 PTO ALEX
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-307-444A-5

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Qy 60 VPGNVTLV-----VGSTSVPLSSPLKVDLVL-----EKEVAGLWI 95
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Qy 96 KIPCTDYIGSCTFEHFCVDLMLIPTGEPCEP-----LRTYGLPCHCPFKEGTYSLPKSE 151
Db 226 --DCSVENGGC--EHACNA-----IPGAPRCQCPAGAALQADGRSCTASATQSCNDLCE-H 276
Qy 152 FAVPDLELPswLTtGNyRIESVLSsSGKRL 181
Db 277 FcVpNPdQP-----GSY---SCMCETGYRL 298
RESULT 13
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; Sequence 5, Application US/08587389
; Patent No. 5695964
; GENERAL INFORMATION:
; APPLICANT: NII, ATSUSHI
; APPLICANT: MORISHITA, HIDEAKI
; APPLICANT: UEMURA, AKIO
; APPLICANT: MOCHIDA, EI
; TITLE OF INVENTION: TRUNCATED THROMBOMODULIN, RECOMBINANT
; TITLE OF INVENTION: PRODUCTION THEREOF, AND THERAPEUTIC AGENT (AS AMENDED)
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/587,389
; FILING DATE: 17-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,444
; FILING DATE: 19-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OLIFF, JAMES A.
; REGISTRATION NUMBER: 27,075
; REFERENCE/DOCKET NUMBER: JAO 27706
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; TELEX: 90-1799 PTO ALEX
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-587-389-5

Query Match 8.1%; Score 82; DB 1; Length 446;
Best Local Similarity 23.3%; Pred. No. 0.8;
Matches 49; Conservative 23; Mismatches 74; Indels 64; Gaps 12;
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Db 117 PLCVAVSAAEATVPSEPIWEEQQCEVKADGFLCEHFH-----PATCRPLAVEPGAAA 168
Qy 60 VPGNVTLV-----VGSTSVPLSSPLKVDLVL-----EKEVAGLWI 95
Db 169 AAVSITYGTPPAARGADFOALPVGSSAA--VAPLGLQLMCTAPPGAVQGHWAREAPGAW- 225
Qy 96 KIPCTDYIGSCTFEHFCVDLMLIPTGEPCEP-----LRTYGLPCHCPFKEGTYSLPKSE 151

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	412	40.5	191	15	US-10-264-049-2611
4	353	34.7	61	9	US-09-864-761-34809
5	162.5	16.0	126	10	US-09-764-891-4977
6	98.5	9.7	273	16	US-10-425-115-297138
7	91.5	9.0	641	15	US-10-369-493-20746
8	90	8.8	651	15	US-10-369-493-20109
9	88	8.6	796	16	US-10-437-963-187458
10	86.5	8.5	196	16	US-10-425-115-251307
11	86.5	8.5	574	16	US-10-725-013-2

12	86.5	8.5	768	9	US-09-973-451-8	Sequence 8, Appli
13	86	8.4	143	9	US-09-860-793-3	Sequence 3, Appli
14	86	8.4	474	15	US-10-369-493-19074	Sequence 19074, A
15	86	8.4	575	15	US-10-094-886-196	Sequence 196, App
16	86	8.4	611	15	US-10-369-493-7417	Sequence 7417, Ap
17	86	8.4	633	15	US-10-369-493-4658	Sequence 4658, Ap
18	86	8.4	2293	16	US-10-032-438B-2	Sequence 2, Appli
19	84	8.3	490	16	US-10-437-963-180789	Sequence 180789,
20	83.5	8.2	132	15	US-10-424-599-255741	Sequence 255741,
21	83	8.2	688	15	US-10-282-122A-47772	Sequence 47772, A
22	82.5	8.1	342	16	US-10-425-115-220322	Sequence 220322,
23	82.5	8.1	342	16	US-10-425-115-220323	Sequence 220323,
24	82.5	8.1	352	15	US-10-425-114-63175	Sequence 63175, A
25	82.5	8.1	371	15	US-10-425-114-62424	Sequence 62424, A
26	82.5	8.1	372	15	US-10-425-114-53454	Sequence 53454, A
27	82.5	8.1	372	15	US-10-425-114-72059	Sequence 72059, A
28	82.5	8.1	375	15	US-10-425-114-58493	Sequence 58493, A
29	82.5	8.1	792	14	US-10-309-422-38	Sequence 38, Appli
30	82.5	8.1	824	16	US-10-467-595-4	Sequence 4, Appli
31	82.5	8.1	926	14	US-10-309-422-36	Sequence 36, Appli
32	82.5	8.1	957	14	US-10-309-422-14	Sequence 14, Appli
33	82.5	8.1	958	14	US-10-309-422-26	Sequence 26, Appli
34	82.5	8.1	1091	14	US-10-309-422-12	Sequence 12, Appli
35	82.5	8.1	1092	14	US-10-309-422-24	Sequence 24, Appli
36	82	8.1	497	15	US-10-298-796-4	Sequence 4, Appli
37	82	8.1	575	9	US-09-938-405-2	Sequence 2, Appli
38	82	8.1	575	14	US-10-150-440-3	Sequence 3, Appli
39	82	8.1	575	14	US-10-438-648-2	Sequence 2, Appli
40	82	8.1	575	15	US-10-410-195-2	Sequence 2, Appli
41	82	8.1	575	15	US-10-373-801-29	Sequence 29, Appli
42	82	8.1	575	17	US-10-785-156-2	Sequence 2, Appli
43	82	8.1	575	18	US-10-712-124-110	Sequence 110, App
44	82	8.1	631	14	US-10-150-440-1	Sequence 1, Appli
45	82	8.1	631	16	US-10-741-601-309	Sequence 309, App

ALIGNMENTS

RESULT 1
US-10-170-385-389
; Sequence 389, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-389

Query Match 98.7%; Score 1005; DB 15; Length 193;
Best Local Similarity 99.0%; Pred. No. 8.8e-97;
Matches 191; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


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; PRIOR APPLICATION NUMBER: PCT/US01/00669
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34809
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011342.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.99
; OTHER INFORMATION: EST HUMAN HIT: BE182886.1, EVALUE 9.00e-34
; OTHER INFORMATION: SWISSPROT HIT: P17900, EVALUE 1.00e-34
; US-09-864-761-34809
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Query Match 34.7%; Score 353; DB 9; Length 61;
Best Local Similarity 100.0%; Pred. No. 3.9e-29;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 VDLVLEKEVAGLWIKIPCTDYIGSCTFEHFCVDLMDLIPTGEPCEPLRTYGLPCHCPFK 141
Db 1 VDLVLEKEVAGLWIKIPCTDYIGSCTFEHFCVDLMDLIPTGEPCEPLRTYGLPCHCPFK 60

Qy 142 E 142
Db 61 E 61

RESULT 5
US-09-764-891-4977
; Sequence 4977, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4977
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (119)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (122)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-4977

Query Match 16.0%; Score 162.5; DB 10; Length 126;
Best Local Similarity 54.2%; Pred. No. 9.2e-09;
Matches 32; Conservative 7; Mismatches 13; Indels 7; Gaps 1;

Qy 13 LGLLLA-----TPQAHLKPKSQLSSFSWDNCFEGKDPVIRSLTLEPDPVIVPGNV 64
Db 24 LGLLLAGPAAHAHVPAHAPVNPQPQVTSFFWENCHERKDPVLLKSNMTLEPDPVIAYPGNV 82

RESULT 6
US-10-425-115-297138
; Sequence 297138, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 297138
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_34069C.1.pep
US-10-425-115-297138

Query Match 9.7%; Score 98.5; DB 16; Length 273;
Best Local Similarity 26.7%; Pred. No. 0.13;
Matches 59; Conservative 24; Mismatches 73; Indels 65; Gaps 14;

Qy 3 SLMQAPL---LIALGLLLATPAQAHKK-----PSQLSSFSWDNCFEGKDPVAVI---RS 50
Db 70 ALLPAALPASLPFAASILYSPLOAVLPRCGISLCFAELAPA--PSCCSSRPPAPLLAWSS 127

Qy 51 LTLEPDPVIVPGNVITLSVVGSTSVPLSSPLKV-----DLVLEKEVAGLW----- 94
Db 128 SFLVPVPCVFP--VTSMAAPSL-PLSSPLRVRLVSSLRRARSFLCVPAATSLWCFLPA 184

Qy 95 -IKIPCTDYIGSCTFEHFCVDLMDLIPTGEPCEPLRTYGLPCH-----CPFKEGTY 145
Db 185 RAKFPCSLALGPC-----STVPCCSARV-KFPCRVLGRKPVCPRR--AC 227

Qy 146 SLPKSEFAVPDLELPSWLTTGNTRIESVLSSSG--KRLGCI 184
Db 228 CSPKR----PMLQRPYFSMSFHVGIIVSVSSSSGINKQTAV 264

RESULT 7
US-10-369-493-20746
; Sequence 20746, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
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Db 5 LVWLAIITLAVVSAGVK-----FQDCKGE-----VESLEVEGSGDYCVIHKGKKL 51

QY 67 SV-VGSTSVPLSSPLKVDLVLEKEVAGLWIKIPCTDYIGSCTFEHFCVDVLDMLIPTGEPC 125

Db 52 DLAISVTSNQDSANLKLDIV--ADINGVQIEVPGVDHDG----- 88

QY 126 PEPLRTYGLPCH---CPFKEGTYSLPKSEFAVPDLELPMSWLTGTGNRYRIESVLSSSGKRLG 182

Db 89 -----CHYVKCPIKKGQHFDVKYTSIPAI-LP---TTKAKIIAKIIGDKGLG-G 133

QY 183 CIKIAASLK 191

Db 134 CIVINGEIQ 142

RESULT 14

US-10-369-493-19074

; Sequence 19074, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 19074

; LENGTH: 474

; TYPE: PRT

; ORGANISM: Anabaena PCC7120

US-10-369-493-19074

Query Match 8.4%; Score 86; DB 15; Length 474;

Best Local Similarity 27.2%; Pred. No. 5.5;

Matches 41; Conservative 22; Mismatches 50; Indels 38; Gaps 10;

QY 68 VVGSTSVPLSSPLKVDLVLEKEVAGLWIKIPCTDYI-----GSCTFEH----PCDVLDM--- 117

Db 228 VIGGERCP-----VDTWQTFETGGIMI-TPLPGAISTKPGSATLPFGILADIVDLEGN 281

QY 118 LIPTGE-----PCPEPLRT-YGLP-----CHCPFKEGTYSLPKSEFAVPDLEL 159

Db 282 TVPENEGGYLAVRYPWPGMMRTVYGDPERFRRTYLGTHPP-KDGNITYFAGDGARKDEDG 340

QY 160 PSWLTGTGNRYRIESVLSSSGKRLGCIKIAASL 190

Db 341 YFWVMG---RVDDVLNVSGHRLGTMEVESAL 368

RESULT 15

US-10-094-886-196

; Sequence 196, Application US/10094886

; Publication No. US20040002120A1

; GENERAL INFORMATION:

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Tchernev, Velizar T.

; APPLICANT: Liu, Xiaohong

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Patturajan, Meera

; APPLICANT: Burgess, Catherine

; APPLICANT: Vernet, Corine A.

; APPLICANT: Li, Li

; APPLICANT: Gorman, Linda

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Boldog, Ferenc

; APPLICANT: Guo, Xiaojia

; APPLICANT: Shenoy, Suresh

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Taupier, Raymond J., Jr.

; APPLICANT: Miller, Charles

; APPLICANT: Casman, Stacie

; APPLICANT: Pena, Carol

; APPLICANT: Gangolli, Esha

; APPLICANT: Gusev, Vladimir

; APPLICANT: Smithson, Glennnda

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Gerlach, Valerie

; APPLICANT: Pochart, Pascal

; APPLICANT: Fernandes, Elma

; APPLICANT: Shimkets, Richard

; APPLICANT: Rastelli, Luca

; APPLICANT: Spaderna, Steven

; APPLICANT: LaRochelelle, William

; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS

; FILE REFERENCE: 21402-290 B

; CURRENT APPLICATION NUMBER: US/10/094,886

; CURRENT FILING DATE: 2002-03-07

; PRIOR APPLICATION NUMBER: 60/274,322

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: 60/313,182

; PRIOR FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: 60/288,052

; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/318,510

; PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/274,281

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: 60/314,018

; PRIOR FILING DATE: 2001-08-21

; PRIOR APPLICATION NUMBER: 60/274,194

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: 60/274,849

; PRIOR FILING DATE: 2001-03-09

; PRIOR APPLICATION NUMBER: 60/296,693

; PRIOR FILING DATE: 2001-06-07

; PRIOR APPLICATION NUMBER: 60/313,626

; PRIOR FILING DATE: 2001-08-21

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 298

; SOFTWARE: PatentIn 2.1

; SEQ ID NO 196

; LENGTH: 575

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-094-886-196

Query Match 8.4%; Score 86; DB 15; Length 575;

Best Local Similarity 23.6%; Pred. No. 7.1;

Matches 49; Conservative 23; Mismatches 76; Indels 60; Gaps 12;

QY 8 PLLIALGLLIAT-----PAQAHLKPSQLSSFSWDNCFEGKDPAVIRSLTLEPDPIV 59

Db 135 PLCVAVSAAEATVPSEPIWEEQQCEVKADGFLCFEHF-----PATCRPLAVEPGAAA 186

QY 60 VPGNVTLVS-----VGSTSVPLSS-----PLKVDLVL-----EKEVAGLWIKI 97

Db 187 AAVSITYGTPTFAARGAGFQALPVGSSAAVAPLGLQMLCTAPPGAVQGHWAREAPGAW--- 243

QY 98 PCTDYIGSCTFEHFCVDVLDMLIPTGEPCPEP----LRTYGLPCHCPFKEGTYSLPKSEFA 153

Db 244 DCSVENGGC--EHTCNA----IPGAPRCQCPAGAALQADGRSCTASATQSCNDLCE-HFC 296

QY 154 VPDLELPMSWLTGTGNRYRIESVLSSSGKRL 181

Db 297 VPNPDPQ-----GSY---SCMCETGYRL 316

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 27, 2005, 19:16:56 ; Search time 512.093 Seconds
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	97.5	9.6	20966	4 US-09-776-976-7	Sequence 7, Appli
2	97.5	9.6	20966	4 US-09-909-547-7	Sequence 7, Appli
3	97.5	9.6	20966	4 US-09-569-852B-1	Sequence 1, Appli
4	92.5	9.1	9950	4 US-09-949-016-12075	Sequence 12075, A
5	92.5	9.1	9950	4 US-09-949-016-14226	Sequence 14226, A
6	92	9.0	99748	4 US-09-949-016-11990	Sequence 11990, A
7	92	9.0	99749	4 US-09-949-016-16518	Sequence 16518, A
8	91	8.9	455726	4 US-09-949-016-14157	Sequence 14157, A
9	91	8.9	481115	4 US-09-949-016-11940	Sequence 11940, A
10	89.5	8.8	890	1 US-08-592-126-78	Sequence 78, Appl
11	89.5	8.8	890	4 US-09-168-595-78	Sequence 78, Appl
12	89.5	8.8	1633	1 US-07-866-979-5	Sequence 5, Appli

C 13	89.5	8.8	1633	2	US-08-466-906B-5	Sequence 5, Appli
C 14	89.5	8.8	1633	3	US-08-706-281A-5	Sequence 5, Appli
C 15	89.5	8.8	1633	3	US-09-201-746-5	Sequence 5, Appli
C 16	89.5	8.8	1633	3	US-09-097-231-5	Sequence 5, Appli
C 17	89.5	8.8	1633	4	US-09-353-099-5	Sequence 5, Appli
C 18	89.5	8.8	1633	4	US-09-016-434-1343	Sequence 1343, Ap
19	88.5	8.7	601	4	US-09-949-016-30962	Sequence 30962, A
20	88.5	8.7	601	4	US-09-949-016-30963	Sequence 30963, A
21	88.5	8.7	601	4	US-09-949-016-158143	Sequence 158143,
22	88.5	8.7	601	4	US-09-949-016-158144	Sequence 158144,
23	88.5	8.7	1388	4	US-09-976-594-806	Sequence 806, App
24	88.5	8.7	22339	4	US-09-949-016-12411	Sequence 12411, A
25	88.5	8.7	22339	4	US-09-949-016-16154	Sequence 16154, A
26	88	8.6	15252	4	US-09-949-016-13584	Sequence 13584, A
27	88	8.6	29485	4	US-09-785-381-6	Sequence 6, Appli
28	88	8.6	43950	3	US-09-735-934A-3	Sequence 3, Appli
29	88	8.6	43950	4	US-10-060-332-3	Sequence 3, Appli
30	88	8.6	43950	4	US-10-339-657-3	Sequence 3, Appli
31	87	8.5	231129	4	US-09-949-016-16110	Sequence 16110, A
32	87	8.5	266293	4	US-09-949-016-11934	Sequence 11934, A
33	86.5	8.5	2781	3	US-09-302-812-7	Sequence 7, Appli
34	86.5	8.5	2781	3	US-09-511-477-7	Sequence 7, Appli
35	86.5	8.5	2781	3	US-09-511-507-7	Sequence 7, Appli
36	86	8.4	588	4	US-09-860-793-2	Sequence 2, Appli
37	86	8.4	29629	3	US-09-729-995-3	Sequence 3, Appli
38	86	8.4	29629	4	US-10-135-689-3	Sequence 3, Appli
39	86	8.4	29629	4	US-10-690-617-3	Sequence 3, Appli
40	86	8.4	37030	4	US-08-311-731A-25	Sequence 25, Appl
41	85.5	8.4	601	4	US-09-949-016-83862	Sequence 83862, A
42	85.5	8.4	1903	6	5466668-5	Patent No. 5466668
43	85.5	8.4	1903	6	5466668-5	Patent No. 5466668
44	85.5	8.4	9805	4	US-09-949-016-13109	Sequence 13109, A
45	85	8.3	2598	4	US-09-949-016-3414	Sequence 3414, Ap

ALIGNMENTS

RESULT 1

US-09-776-976-7
; Sequence 7, Application US/09776976
; Patent No. 6566332
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76.US4.REG
; CURRENT APPLICATION NUMBER: US/09/776,976
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/758,055
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/176,228
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/198,087
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/299,881
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO 7
; LENGTH: 20966
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..4811
; OTHER INFORMATION: 5' regulatory region
; NAME/KEY: exon
; LOCATION: 4812..4851
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 15144..15365

OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 16277..20559
OTHER INFORMATION: exon 3
NAME/KEY: misc feature
LOCATION: 20560..20966
OTHER INFORMATION: 3' regulatory region
NAME/KEY: allele
LOCATION: 3787
OTHER INFORMATION: 9-27-261 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 11118
OTHER INFORMATION: 99-14387-129 : polymorphic base A or C
NAME/KEY: allele
LOCATION: 15120
OTHER INFORMATION: 9-12-48 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 15196
OTHER INFORMATION: 9-12-124 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 15427
OTHER INFORMATION: 9-12-355 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 15500
OTHER INFORMATION: 9-12-428 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 15863
OTHER INFORMATION: 99-14405-105 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 17170
OTHER INFORMATION: 9-16-189 : polymorphic base deletion of A
NAME/KEY: primer_bind
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LOCATION: 15759..15776
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LOCATION: 15481..15499
OTHER INFORMATION: 9-12-428.mis
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NAME/KEY: primer_bind
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OTHER INFORMATION: 99-14405-105.mis complement
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LOCATION: 17151..17169
OTHER INFORMATION: 9-16-189.mis
NAME/KEY: primer_bind
LOCATION: 17171..17189
OTHER INFORMATION: 9-16-189.mis complement
US-09-776-976-7

Alignment Scores:
Pred. No.: 7.68 Length: 20966
Score: 97.50 Matches: 57
Percent Similarity: 41.75% Conservative: 24
Best Local Similarity: 29.38% Mismatches: 72
Query Match: 9.58% Indels: 41
DB: 4 Gaps: 10

US-10-030-937-9 (1-193) x US-09-776-976-7 (1-20966)

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Db 6579 ACTCAGCCTGGCAAAAGAGCAAACTCCATCTCAAAAAAATAAGACACA 6638
Qy 34 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArgSerLeuThrLeu 53
Db 6639 AGACTGGCTCCTTGTCTTTTGGGA-----CAGGGTCTCACTCTA 6680
Qy 54 GluProAspProIleValValProGlyAsnValThr-----LeuSerValVal 69
Db 6681 TCACCC---AGGCTGGAGTGCAGTGTGCAATCACAGCTCACTGCAGCCTCGATTCCCA 6737
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Db 6738 GGCTCAAGTGACCCCTCCCATCTTAGCTCCTGAGTGTGGACTACAGGTGTGTGCAAC 6797
Qy 89 uValAlaGlyLeuTrpIleLysIleProCysThrAspTyrIleGlySerCysThrPheG1 109
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Qy 109 uHisPheCysAspValLeuAspMetLeuIleProThrGlyGluProCysProGluProLe 129
Db 6847 -TATGGCTGGGGGCTCAAACTCCTGGGCTCAGCAGTCTCCCA---CCTCAGCCTCC 6902
Qy 129 uArgThrTyrGlyLeu---ProCysHis-----CysProPheLysGluGlyTh 144
Db 6903 CAAAAGCTGGGATATATATGCTTGCTCTTTTAAGTGGCTGTAGGGACAAACTTCCAC 6962
Qy 144 rTyrSerLeuProLys-SerGluPheAlaValProAspLeuGluLeuProSer----- 161
Db 6963 CTACTCCTTGTCAAGCCAGTGGACCGGTGGTCCCAACATACCGGTAAAGTCAAGAGGTG 7022
Qy 162 -----TrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyL 179
Db 7023 ATGTCTTTTGGAGAGATACTTTTCAATCAGGAATTTCAATCAGAAATTCATCATGTGGAG 7082
Qy 179 ysArgLeu-----GlyCys 183
Db 7083 AGAGACTTATCTTAAATAATGTGGTGGTGGTGGATGC 7120

RESULT 2
US-09-909-547-7
; Sequence 7, Application US/09909547
; Patent No. 6579852
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Bihaun, Bernard
; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76.US6.CIP
; CURRENT APPLICATION NUMBER: US/09/909,547
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/776,976
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/758,055
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/299,881
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 60/198,087
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/176,228
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO 7
; LENGTH: 20966
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..4811
; OTHER INFORMATION: 5' regulatory region
; NAME/KEY: exon

; LOCATION: 4812..4851
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 15144..15365
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: 16277..20559
; OTHER INFORMATION: exon 3
; NAME/KEY: misc feature
; LOCATION: 20560..20966
; OTHER INFORMATION: 3' regulatory region
; NAME/KEY: allele
; LOCATION: 3787
; OTHER INFORMATION: 9-27-261 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 11118
; OTHER INFORMATION: 99-14387-129 : polymorphic base A or C
; NAME/KEY: allele
; LOCATION: 15120
; OTHER INFORMATION: 9-12-48 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 15196
; OTHER INFORMATION: 9-12-124 : polymorphic base G or T
; NAME/KEY: allele
; LOCATION: 15427
; OTHER INFORMATION: 9-12-355 : polymorphic base G or T
; NAME/KEY: allele
; LOCATION: 15500
; OTHER INFORMATION: 9-12-428 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 15863
; OTHER INFORMATION: 99-14405-105 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 17170
; OTHER INFORMATION: 9-16-189 : polymorphic base deletion of A
; NAME/KEY: primer_bind
; LOCATION: 3528..3545
; OTHER INFORMATION: 9-27.pu
; NAME/KEY: primer_bind
; LOCATION: 3928..3946
; OTHER INFORMATION: 9-27.rp complement
; NAME/KEY: primer_bind
; LOCATION: 10990..11008
; OTHER INFORMATION: 99-14387.pu
; NAME/KEY: primer_bind
; LOCATION: 11423..11442
; OTHER INFORMATION: 99-14387.rp complement
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; LOCATION: 15073..15092
; OTHER INFORMATION: 9-12.pu
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; LOCATION: 15503..15520
; OTHER INFORMATION: 9-12.rp complement
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; LOCATION: 15759..15776
; OTHER INFORMATION: 99-14405.pu
; NAME/KEY: primer_bind
; LOCATION: 16191..16211
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; OTHER INFORMATION: 9-27-261.probe
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; LOCATION: 11106..11130
; OTHER INFORMATION: 99-14387-129.probe
; NAME/KEY: misc binding
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; OTHER INFORMATION: 9-12-48.probe
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; NAME/KEY: primer_bind
; LOCATION: 3788..3806
; OTHER INFORMATION: 9-27-261.mis complement
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; LOCATION: 11099..11117
; OTHER INFORMATION: 99-14387-129.mis
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; LOCATION: 15101..15119
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; LOCATION: 15121..15139
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; LOCATION: 15177..15195
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; OTHER INFORMATION: 9-12-124.mis complement
; NAME/KEY: primer_bind
; LOCATION: 15408..15426
; OTHER INFORMATION: 9-12-355.mis
; NAME/KEY: primer_bind
; LOCATION: 15428..15446
; OTHER INFORMATION: 9-12-355.mis complement
; NAME/KEY: primer_bind
; LOCATION: 15481..15499
; OTHER INFORMATION: 9-12-428.mis
; NAME/KEY: primer_bind
; LOCATION: 15501..15519
; OTHER INFORMATION: 9-12-428.mis complement
; NAME/KEY: primer_bind
; LOCATION: 15844..15862
; OTHER INFORMATION: 99-14405-105.mis
; NAME/KEY: primer_bind
; LOCATION: 15864..15882
; OTHER INFORMATION: 99-14405-105.mis complement
; NAME/KEY: primer_bind
; LOCATION: 17151..17169
; OTHER INFORMATION: 9-16-189.mis
; NAME/KEY: primer_bind
; LOCATION: 17171..17189
; OTHER INFORMATION: 9-16-189.mis complement
; US-09-909-547-7
;
; Alignment Scores:
; Pred. No.: 7.68 Length: 20966
; Score: 97.50 Matches: 57
; Percent Similarity: 41.75% Conservative: 24
; Best Local Similarity: 29.38% Mismatches: 72
; Query Match: 9.58% Indels: 41
; DB: 4 Gaps: 10
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US-10-030-937-9 (1-193) x US-09-909-547-7 (1-20966)
QY 19 ThrProAlaGlnAla-----HisLeuLysLysProSerGlnLeuSerSer 33
Db 6579 ACTCCAGCCTGGGCAAAAAGAGCAAAACTCCATCTCAAAAAAATAAGACACA 6638
QY 34 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArgSerLeuThrLeu 53
Db 6639 AGACTGGCTCCTTCTCTTTTGGGGA-----CAGGGTCTCACTCTA 6680
QY 54 GluProAspProIleValValProGlyAsnValThr-----LeuSerValVal 69
Db 6681 TCACCC--AGGCTGGAGTGCAGTGGTGCAATCAGACTCACTGCAGCCTCGATTTCCCA 6737
QY 70 GlySerThrSerValProLeuSerSer-ProLeuLysValAspLeuValLeuGluLysGl 89
Db 6738 GGCTCAAGTGACCCCTCCCATCTTAGCCTCCTAGTAGCTGGGACTACAGGTGTGTGCAAC 6797
QY 89 uValAlaGlyLeuTrpIleLysIleProCysThrAspTyrIleGlySerCysThrPheGl 109
Db 6798 CATGCCTGGCTAATTTTAAAAATTTTGTAGAGATGAGGTCTCACTA----- 6846
QY 109 uHisPheCysAspValLeuAspMetLeuIleProThrGlyGluProCysProGluProLe 129
Db 6847 -TATTGGCTGGGGGCGCTCAAACTCCTGGGCTCAGCAGTCCCTCCA---CCTCAGCCTCC 6902
QY 129 uArgThrTyrGlyLeu---ProCysHis-----CysProPheLysGluGlyTh 144
Db 6903 CAAAAGGCTGGGATATATATGCTTGTCTTTTAAAGTGGCTGTAGGACAAAACTTTCCAC 6962
QY 144 rTyrSerLeuProLys-SerGluPheAlaValProAspLeuGluLeuProSer----- 161
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QY 162 -----TipLeuThrThrGlyAanTyrArgIleGluSerValLeuSerSerSerGlyL 179
Db 7023 ATGTCTTTTGGAGAGATACTTTCAATCAGGAATTTCAATCAGAAATTCATATCATGTGGAG 7082
QY 179 ysArgLeu-----GlyCys 183
Db 7083 AGAGACTTATCCTAAAAATGTGGTGGTGGTGGATGC 7120
RESULT 3
US-09-569-852B-1
; Sequence 1, Application US/09569852B
; Patent No. 6582909
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Denison, Blake
; APPLICANT: Yen-Potin, Frances
; TITLE OF INVENTION: APM1 Biallelic Markers and Uses Thereof
; FILE REFERENCE: GEN-T113XC2
; CURRENT APPLICATION NUMBER: US/09/569,852B
; PRIOR APPLICATION NUMBER: PCT/IB99/01858
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: US 09/434,848
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: US 60/119,593
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/107,113
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20966
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(4811)
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; NAME/KEY: primer_bind
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; OTHER INFORMATION: 17-37-629.mis
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; OTHER INFORMATION: 17-37-629.mis complement
; NAME/KEY: primer_bind
; LOCATION: (17992)..(18010)
; OTHER INFORMATION: 17-37-811.mis
; NAME/KEY: primer_bind
; LOCATION: (18012)..(18030)
; OTHER INFORMATION: 17-37-811.mis complement
; NAME/KEY: primer_bind
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; OTHER INFORMATION: 17-38-349.mis
; NAME/KEY: primer_bind
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; LOCATION: (946)..(964)
; OTHER INFORMATION: 17-30-216.mis complement
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; OTHER INFORMATION: 9-27-246.mis complement
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; OTHER INFORMATION: 9-27-261.mis
; NAME/KEY: primer_bind
; LOCATION: (3788)..(3806)
; OTHER INFORMATION: 9-27-261.mis complement
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; NAME/KEY: primer_bind
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; LOCATION: (11020)..(11038)
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; NAME/KEY: primer_bind
; LOCATION: (11040)..(11058)
; OTHER INFORMATION: 99-14387-50.mis complement
; NAME/KEY: primer_bind
; LOCATION: (11099)..(11117)
; OTHER INFORMATION: 99-14387-129.mis
; NAME/KEY: primer_bind
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LOCATION: (11119)..(11137)
OTHER INFORMATION: 99-14387-129.mis complement
NAME/KEY: primer bind
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OTHER INFORMATION: 99-14387-199.mis
NAME/KEY: primer bind
LOCATION: (11189)..(11207)
OTHER INFORMATION: 99-14387-199.mis complement
NAME/KEY: primer bind
LOCATION: (13954)..(13972)
OTHER INFORMATION: 17-33-TGAGACT.mis
NAME/KEY: primer bind
LOCATION: (13974)..(13992)
OTHER INFORMATION: 17-33-TGAGACT.mis complement
NAME/KEY: exon
LOCATION: (4812)..(4851)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (15144)..(15365)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (16277)..(20559)
OTHER INFORMATION:
NAME/KEY: misc feature
LOCATION: (20560)..(20966)
OTHER INFORMATION: 3' regulatory region

Alignment Scores:
Pred. No.: 7.68 Length: 20966
Score: 97.50 Matches: 57
Percent Similarity: 41.75% Conservative: 24
Best Local Similarity: 29.38% Mismatches: 72
Query Match: 9.58% Indels: 41
DB: 4 Gaps: 10

US-10-030-937-9 (1-193) x US-09-569-852B-1 (1-20966)

QY 19 ThrProAlaGlnAla-----HisLeuLysLysProSerGlnLeuSerSer 33
Db 6579 ACTCCAGCCTGGGCAAAAGAGCAAAACTCCATCTCAAAAAAAAAAAAAATAGACACA 6638
QY 34 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArgSerLeuThrLeu 53
Db 6639 AGACTGGCTCCTGTCTTTTGGGGA-----CAGGGTCTCACTCTA 6680
QY 54 GluProAspProIleValValProGlyAsnValThr-----LeuSerValVal 69
Db 6681 TCACCC---AGGCTGGAGTGCAGTGGTGAATCACAGCTCACTGCAGCCTCGATTCCCA 6737
QY 70 GlySerThrSerValProLeuSerSer-ProLeuLysValAspLeuValLeuGluLysGl 89
Db 6738 GGCTCAAGTGACCCTCCCATCTAGCCTCCTGAGTAGCTGGGACTACAGGTGTGTGAAC 6797
QY 89 uValAlaGlyLeuTrpIleLysIleProCysThrAspTyrIleGlySerCysThrPheGl 109
Db 6798 CATGCCCTGGCTAAATTTTAAAAATTTTGTAGAGATGAGTCTCACTA----- 6846
QY 109 uHisPheCysAspValLeuAspMetLeuIleProThrGlyGluProCysProGluProLe 129
Db 6847 -TATTGGCTGGGGGCTCAAACTCCTGGGCTCAGCAGTCTCTCCCA---CCTCAGCCTCC 6902
QY 129 uArgThrTyrGlyLeu---ProCysHis-----CysProPheLysGluGlyTh 144
Db 6903 CAAAAGGCTGGGATTATATGCTTCTTTTAAAGGTGGCTGTAGGGACAAACTTTCCAC 6962
QY 144 rTyrSerLeuProLys-SerGluPheAlaValProAspLeuGluLeuProSer----- 161
Db 6963 CTACTCCTTGCAAGCCAGTGGACCGGTGGTGGTCCAGACATACGGCTAAAGTCAAGAGGTG 7022
QY 162 -----TrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyL 179
Db 7023 ATGCTTTTGGAGAGATACCTTTCAATCAGGAATTTCAATCAGAAATTCATCATGTGGAG 7082

QY 179 ysArgLeu-----GlyCys 183
Db 7083 AGAGACTTATCCTAAAAATGTGGTGGTGGTGGATGC 7120
RESULT 4
US-09-949-016-12075
; Sequence 12075, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12075
; LENGTH: 9950
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12075
Alignment Scores:
Pred. No.: 9.26 Length: 9950
Score: 92.50 Matches: 50
Percent Similarity: 36.53% Conservative: 30
Best Local Similarity: 22.83% Mismatches: 78
Query Match: 9.09% Indels: 61
DB: 4 Gaps: 11

US-10-030-937-9 (1-193) x US-09-949-016-12075 (1-9950)

QY 4 LeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrProAlaGlnAla 23
Db 4397 CTCCTTCCTGCCCCCTGTGC-----ACCTCCCT 4426
QY 24 HisLeuLysLysProSerGlnLeu-----SerSerPheSerTrpAsp 37
Db 4427 AACTATGGGTCCCAACACAGGTTCTCGGCAGCGAGTGGCTACGTCAATTGTGGTC 4486
QY 38 AsnCysPheGluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspPro 57
Db 4487 TCACGTGTC-----GACCCCTTTATATTGTGGCAGCCTCACAGTGCATCACCC 4537
QY 58 IleValVal----- 60
Db 4538 CTTCTTGTCTTCCCGTGGCCTTCCAGCGTCATTGCCGGGCTTCCCTCTCCTTCCGGCTA 4597
QY 61 ---ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerPro 79
Db 4598 AGCCCACTGTGGTGTCTGAGCCTCCTCAGCTCATCA-----CCTTATTCTGCTCCT 4651
QY 80 -----LeuLysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLys 96
Db 4652 TAGCACTCTATGAGCCAGACCATCTCCTGAATTCTTCTGCCTCC----- 4696
QY 97 IleProCysThrAspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAsp 116
Db 4697 CTTCTTGACAGCCCAAGCACTCCCTCC---CCACTGCAGCACCCAGCTTTAACTTTGGGT 4753
QY 117 MetLeuIleProThrGlyGluProCysProGluProLeuArgThrTyr----- 132
Db 4754 TTTCTTTTCTTCTTCAGGCTGGAGCCCCCAACTCCCTTGACAGGTGACGCTGGAGCAGGT 4813
QY 133 -----GlyLeuProCysHisCysProPheLysGluGlyThrTyrSerLeuProLys 149

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Db 4814 TCCAGGTGGGGCTGCCCTGCCCTGCTGCTGGTGGGGACCCGGTCTTTCTCTCACT 4873
Qy 150 SerGluPheAlaValProAspLeuGluLeuProSerTrpLeuThrThrGlyAsn----- 167
Db 4874 GCCAAGTGGACTCCTCTCTGGG---GGAGGCCCTGACTCTGCTGGTGGAGACAATGGC 4930
Qy 168 -----TyrArgIleGluSerValLeuSerSerGlyLysArgLeuGlyCys 183
Db 4931 GACTTTACCTTCGACTAGAGGATGTGAGCCAGGCCAGGCTGGGACCTACACCTGC 4987
RESULT 5
US-09-949-016-14226
; Sequence 14226, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14226
; LENGTH: 9950
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14226
Alignment Scores:
Pred. No.: 9.26 Length: 9950
Score: 92.50 Matches: 50
Percent Similarity: 36.53% Conservative: 30
Best Local Similarity: 22.83% Mismatches: 78
Query Match: 9.09% Indels: 61
DB: 4 Gaps: 11
US-10-030-937-9 (1-193) x US-09-949-016-14226 (1-9950)
Qy 4 LeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrProAlaGlnAla 23
Db 4397 CTCCTCTCCTGCCCCCTTGTC-----ACCTCCCT 4426
Qy 24 HisLeuLysLysProSerGlnLeu-----SerSerPheSerTrpAsp 37
Db 4427 AACTATGGGTCCCAACACAGGTTCTCGGCAGCAGTGGCCTACGTCATTGCTGGGTC 4486
Qy 38 AsnCysPheGluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspPro 57
Db 4487 TCACTGTTTC-----GACCCCTTTATATTGCTGGCAGCCTCACAGCTGCCATCACCC 4537
Qy 58 IleValVal----- 60
Db 4538 CTTCTGTCTTCTCCGTTGGCTTCCAGCGTCATTGCGCGGCTTCCCTCTCTCCGGCTA 4597
Qy 61 ---ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerPro 79
Db 4598 AGCCCACTTGCTGGGTTCTGAGCCTCTCAGTCATCA-----CCTATTCTGCTCCT 4651
Qy 80 -----LeuLysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLys 96
Db 4652 TAGCACTCTTATGAGCCAGACCATCTCTGAAATTTCTTCTGCCTCC----- 4696
Qy 97 IleProCysThrAspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAsp 116
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Qy 117 MetLeuIleProThrGlyGluProCysProGluProLeuArgThrTyr----- 132
Db 4754 TTTCTTTTCTCTCAGGTCTGGAGCCCCCAACTCCCTTGACAGTGTACGCTGGAGCAGGT 4813
Qy 133 -----GlyLeuProCysHisCysProPheLysGluGlyThrTyrSerLeuProLys 149
Db 4814 TCCAGGTGGGGCTGCCCTGCCCTGCTGCTGGTGGGGACCCGGTCTTTCTCTCACT 4873
Qy 150 SerGluPheAlaValProAspLeuGluLeuProSerTrpLeuThrThrGlyAsn----- 167
Db 4874 GCCAAGTGGACTCCTCTCTGGG---GGAGGCCCTGACTCTCTGCTGGAGACAATGGC 4930
Qy 168 -----TyrArgIleGluSerValLeuSerSerGlyLysArgLeuGlyCys 183
Db 4931 GACTTTACCTTCGACTAGAGGATGTGAGCCAGGCCAGGCTGGGACCTACACCTGC 4987
RESULT 6
US-09-949-016-11990
; Sequence 11990, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11990
; LENGTH: 99748
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11990
Alignment Scores:
Pred. No.: 505 Length: 99748
Score: 92.00 Matches: 52
Percent Similarity: 40.22% Conservative: 22
Best Local Similarity: 28.26% Mismatches: 56
Query Match: 9.04% Indels: 54
DB: 4 Gaps: 12
US-10-030-937-9 (1-193) x US-09-949-016-11990 (1-99748)
Qy 5 MetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrProAlaGlnAlaHis 24
Db 77933 CTGGCCTCACCTCTCTGGTTCTGGGCTCACTCTCTCCAGCCTCACCTCTCTGGTT--- 77989
Qy 25 LeuLysLysProSerGlnLeuSerSerPheSerTrpAspAsnCysPheGluGlyLysAsp 44
Db 77990 -----CCTCGGTCACTCTCTCCAGCCTCA-----CCC 78016
Qy 45 ProAlaValIleArgSerLeuThrLeuGluProAspProIleValValProGlyAsnVal 64
Db 78017 CCTCTGGTTCTCTCGCTCACTCTCTCTGGCCTCACTCTCTG---ATTCTGGCTCACTC 78073
Qy 65 -----ThrLeuSerValValGlySerThrSerVal 74
Db 78074 TCTCCAGCTTCAACCCCTCCGGTCTCTCGCTCACTATCTCCAGTCTCAACCTCTCTGGTT 78133
Qy 75 Pro--LeuSerSerProLeuLysValAspLeuValLeuGluLysGluValAlaGlyLeu 94
Db 78134 CCTGGCTCACTTCTCCAGCCTCACTG-----GCCTCTCTCACTGT 78172
Qy 94 rPileLysIleProCysThrAspTyr---IleGlySerCys-----ThrPheGluH 110
```

Db 78173 GCTGACACACACCGTGATTCTCATGAACCTGGCATGTGCCATTCCCTCTGCCAGGAAC 78232
Qy 110 isPheCysAspValLeuAspMetLeuIleProThr-----GlyGluProCysProG 127
Db 78233 ATTTC-----CTCCCAAGCCTCCCATGGCTCACTCTGCCCTG 78271
Qy 127 luProLeuArgThrTyrGlyLeuProCysHisCysProPheLysGluGlyThrTyrSerL 147
Db 78272 TACACTGTGCCCCACTGTGCATGCTCCCTGCCAC--CCTGTCTAGGTTCTTCTAGTCT 78328
Qy 147 euProLysSerGluPheAlaVal-----ProAspLeu-----GluLeuP 160
Db 78329 TGCCACCATCAGACACAGCACTGTGCACCCCTGAGCTGATCTCCCTCGGCAGTCAGCTCC 78388
Qy 160 roSerTrp 162
Db 78389 CAGGGTGG 78396

RESULT 7
US-09-949-016-16518
; Sequence 16518, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16518
; LENGTH: 99749
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16518

Alignment Scores:
Pred. No.: 505 Length: 99749
Score: 92.00 Matches: 52
Percent Similarity: 40.22% Conservative: 22
Best Local Similarity: 28.26% Mismatches: 56
Query Match: 9.04% Indels: 54
DB: 4 Gaps: 12

US-10-030-937-9 (1-193) x US-09-949-016-16518 (1-99749)
Qy 5 MetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrProAlaGlnAlaHis 24
Db 77933 CTGGCCTCAGCTCCTCTGGTTCCTGGCTCACTCTCTCCAGCCTCACCTCCTCTGGTT--- 77989
Qy 25 LeuLysLysProSerGlnLeuSerSerPheSerTrpAspAsnCysPheGluGlyLysAsp 44
Db 77990 -----CCTCGGTCACTCTCTCCAGCCTCA-----CCC 78016
Qy 45 ProAlaValIleArgSerLeuThrLeuGluProAspProIleValValProGlyAsnVal 64
Db 78017 CCTCTGGTTCTCGTCACTCTCTCTGGCCTCACCTCCTCTG---ATTCTGGCTCACTC 78073
Qy 65 -----ThrLeuSerValValGlySerThrSerVal 74
Db 78074 TCTCCAGCTTCACCCCTCCGGTTCTCTCGTCACTATCTCCAGTCTCAACCTCTCTGGTT 78133
Qy 75 Pro--LeuSerSerProLeuLysValAspLeuValLeuGluLysGluValAlaGlyLeuT 94
Db 78134 CTGGCTCACTTCTCCAGCCTCACTG-----GCCTCTTCACTGT 78172

Qy 94 rpIleLysIleProCysThrAspTyr---IleGlySerCys-----ThrPheGluH 110
Db 78173 GCTGACACACACCGTGATTCTCATGAACCTGGCATGTGCCATTCCCTCTGCCAGGAAC 78232
Qy 110 isPheCysAspValLeuAspMetLeuIleProThr-----GlyGluProCysProG 127
Db 78233 ATTTC-----CTCCCAAGCCTCCCATGGCTCACTCTGCCCTG 78271
Qy 127 luProLeuArgThrTyrGlyLeuProCysHisCysProPheLysGluGlyThrTyrSerL 147
Db 78272 TACACTGTGCCCCACTGTGCATGCTCCCTGCCAC--CCTGTCTAGGTTCTTCTAGTCT 78328
Qy 147 euProLysSerGluPheAlaVal-----ProAspLeu-----GluLeuP 160
Db 78329 TGCCACCATCAGACACAGCACTGTGCACCCCTGAGCTGATCTCCCTCGGCAGTCAGCTCC 78388
Qy 160 roSerTrp 162
Db 78389 CAGGGTGG 78396

RESULT 8
US-09-949-016-14157/c
; Sequence 14157, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14157
; LENGTH: 455726
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(455726)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14157

Alignment Scores:
Pred. No.: 8.53e+03 Length: 455726
Score: 91.00 Matches: 51
Percent Similarity: 37.50% Conservative: 21
Best Local Similarity: 26.56% Mismatches: 77
Query Match: 8.94% Indels: 44
DB: 4 Gaps: 7

US-10-030-937-9 (1-193) x US-09-949-016-14157 (1-455726)
Qy 2 GlnSerLeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrProAla 21
Db 103381 CAGAGCCTTCAGTTCTCACCCCTCTGCCTCCTGCTTCTATCATGAAGCCACACAGCC 103322
Qy 22 GlnAlaHisLeuLysLysProSerGlnLeu--SerSerPheSerTrpAspAsn----- 38
Db 103321 TCTCACCCGGAAAGCAGCCCGCCCTGCGAGCCTCTGCTCCATCGGACAATACCCCA 103262
Qy 39 ---CysPheGluGlyLysAspProAlaValIleArgSerLeuThr----- 52
Db 103261 CAGTGTGGCAAGGCTCGGTCCACTTCCACAGACCCCTCCTCACTCCCACTGCAGCC 103202
Qy 53 ---LeuGluProAspProIleVal-ValProGlyAsnValThrLeuSerValValGlySe 71

Db 103201 TGACTCGGCGCCGACACAGCTCTGTCTCCTGCCAAGGCCACGATG----- 103156
Qy 71 rThrSerValProLeuSerSerProLeuLysValAspLeuValLeuGluLysGluValAl 91
Db 103155 -ACTTCAGG-CTGTTCTCAAGTGGCCTTCTGTATGACACTTTGGCCACCTCACCTCTGGG 103098
Qy 91 aGlyLeuTrpIleLysProCysThrAspTyrIleGlySerCysThrPheGluHisPh 111
Db 103097 GCACGGCTGGCCCTCACTCCAGGGTGGCCACCTGCTCTCCACCCCTCTCCAG----- 103043
Qy 111 eCysAspValLeuAspMetLeuIleProThrGlyGluProCys-ProGluProLeuArgT 131
Db 103042 -----CTCCCTGCGCAGGGCCTGCTCCCGCAGCCCTTGCCT 103005
Qy 131 hr-----TyrGlyLeuProCysHisCysPropheLysGluGlyThrTyrSerLeuProL 149
Db 103004 GTGGGTTCCTCGGGTCCCTCCACATATCCACAAGGACCTCACCTCTGCTGCCATGCCAA 102945
Qy 149 ysSerGluPheAlaValProAspLeuGluLeu----- 159
Db 102944 TGACTCCCAATTCTGATCCATCTCCAGGGCTCCCTTCTCTGAGCCCAACACCCACAC 102885
Qy 160 -----ProSerTrpLeuThr 164
Db 102884 CCCACACCCACCGGGGTCCACCCCTGGCTGACC 102853

RESULT 9
US-09-949-016-11940/c
; Sequence 11940, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11940
; LENGTH: 481115
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(481115)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11940

Alignment Scores:
Pred. No.: 9.34e+03 Length: 481115
Score: 91.00 Matches: 51
Percent Similarity: 37.50% Conservative: 21
Best Local Similarity: 26.56% Mismatches: 77
Query Match: 8.94% Indels: 44
DB: 4 Gaps: 7

US-10-030-937-9 (1-193) x US-09-949-016-11940 (1-481115)

Qy 2 GlnSerLeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrProAla 21
Db 80770 CAGAGCCTTCAGTTCTCACCCCTCTGCTCTCTATCATGAAGCCACACGACC 80711
Qy 22 GlnAlaHisLeuLysLysProSerGlnLeu---SerSerPheSerTrpAspAsn----- 38
Db 80710 TCTCACCGGAAAGCAGACCCCGCCGAGCCTCTGCTCCATCGGACAATACCCCA 80651

Qy 39 ---CysPheGluGlyLysAspProAlaValIleArgSerLeuThr----- 52
Db 80650 CAGTGTGGCAAGCCTGCGTCCACTTCCACACGACCCCTCTCCTACTCCACTGCAGCC 80591
Qy 53 ---LeuGluProAspProIleVal-ValProGlyAsnValThrLeuSerValValGlySe 71
Db 80590 TGACTCCGCGCCGACACAGCTCTGTCTCTGCCAAGGCCACGATG----- 80545
Qy 71 rThrSerValProLeuSerSerProLeuLysValAspLeuValLeuGluLysGluValAl 91
Db 80544 -ACTTCAGG-CTGTTCTCAAGTGGCCTTCTGTATGACACTTTGGCCACCTCACCTCTGGG 80487
Qy 91 aGlyLeuTrpIleLysProCysThrAspTyrIleGlySerCysThrPheGluHisPh 111
Db 80486 GCACGGTGGCCCTCACTCCAGGGTGGCCACCTGCTCTCCACCCCTCTCCAG----- 80432
Qy 111 eCysAspValLeuAspMetLeuIleProThrGlyGluProCys-ProGluProLeuArgT 131
Db 80431 -----CTCCCTGCGCAGGGCCTGCTCCCGCAGCCCTTGCCT 80394
Qy 131 hr-----TyrGlyLeuProCysHisCysPropheLysGluGlyThrTyrSerLeuProL 149
Db 80393 GTGGGTTCCTCGGGTCCCTCCACATATCCACAAGGACCTCACCTCTGCTGCCATGCCAA 80334
Qy 149 ysSerGluPheAlaValProAspLeuGluLeu----- 159
Db 80333 TGACTCCCAATTCTGATCCATCTCCAGGGCTCCCTTCTCTGAGCCCAACACCCACAC 80274
Qy 160 -----ProSerTrpLeuThr 164
Db 80273 CCCACACCCACCGGGGTCCACCCCTGGCTGACC 80242

RESULT 10
US-08-592-126-78
; Sequence 78, Application US/08592126
; Patent No. 5821091
; GENERAL INFORMATION:
; APPLICANT: Gregory Dolganov
; TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
; TITLE OF INVENTION: Polypeptides
; NUMBER OF SEQUENCES: 151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,126
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 4600-0111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 890 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

```
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: G256.seq
US-08-592-126-78

Alignment Scores:
Pred. No.: 0.386 Length: 890
Score: 89.50 Matches: 53
Percent Similarity: 39.89% Conservative: 22
Best Local Similarity: 28.19% Mismatches: 67
Query Match: 8.79% Indels: 47
DB: 1 Gaps: 10

US-10-030-937-9 (1-193) x US-08-592-126-78 (1-890)
QY 3 SerLeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuLeuAlaThrProAlaGln 22
Db 49 TCCCTTTACCAAAAGCCCTA-----CCCATGGGTGGGTGAGGAGGCCCAAGACAG 102
QY 23 AlaHisLeuLysLysProSerGlnLeuSerSerPheSer---TrpAspAsnCysPheGlu 41
Db 103 GCCCGTATCAGGAGGACCCCTCTCTCAGGGGGTGCCCTCTGGGATAAC-----153
QY 42 GlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValPro 61
Db 154 -----CACCCCGCCCTCTTGGGTTTCCT 177
QY 62 GlyAsnValThrLeuSerValValGlySerThrSerVal-----74
Db 178 GCTTCCTAT---CTGGCTGCAGTTTCTCAGGTCCCTTGTGGATTTCCTCATGGTCTGTCC 234
QY 75 ProLeuSerSerProLeuLysValAspLeuValLeuGluLysGluValAlaGlyLeuTrp 94
Db 235 CCACTCACATCCCTCTCTGCAAAACCTTGCTACTG-----GGCCTGCAC 279
QY 95 IleLysIleProCysThrAspTyrIleGlySerCysThrPheGluHisPheCysAspVal 114
Db 280 CTGGCAAATCCATGCTCAGCACAGACGGGATCAAGACCTCTCAATACAACGT-----333
QY 115 LeuAspMetLeuIleProThrGlyGluProCysProGluProLeuArgThrTyrGlyLeu 134
Db 334 -----CTCCTGCCAAT-----CCCTGCCCGCAGCAGCCTGAGGCCAGTCTGAAA 377
QY 135 ProCysHisCys---ProPheLysGlu-GlyThrTyrSerLeuProLysSerGluPheAl 153
Db 378 CCAGGGAGTTGCTCTCTCTTCTCCTCCCTGACCTCACCCCTCAGACCATGCTCAAGTAC 497
QY 153 aValProAspLeu-----GluLeuProSerTrpLeuThrThrGlyAs 167
Db 438 CCTCCTAAACCTCCAGGCCAGCCCTCCCGCAGCTCCAGTGACAGTGCTCCTCAGGTAC 497
QY 167 nTyrArgIleGluSerValLeu 174
Db 498 CTGAGCTCAGCTCTCGGTGCTA 519

RESULT 11
US-09-168-595-78
; Sequence 78, Application US/09168595
; Patent No. 6555666
; GENERAL INFORMATION:
; APPLICANT: Gregory Dolganov
; TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
; TITLE OF INVENTION: Polypeptides
; NUMBER OF SEQUENCES: 151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```


Db 438 CCTCTAAACCTCCAGGCGAGCCCTCTCCAGTCCAGTGACAGTGTCTCTCAGGTAC 497

QY 167 nTyArgIleGluSerValLeu 174

Db 498 CTGAGCTCAGCTCTCGGTGCTA 519

RESULT 12

US-07-866-979-5/c

; Sequence 5, Application US/07866979

; Patent No. 5532347

; GENERAL INFORMATION:

; APPLICANT: Cone, Roger D

; APPLICANT: Mountjoy, Kathleen G

; TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor

; TITLE OF INVENTION: and Uses

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Allegretti & Witcoff, Ltd.

; STREET: 10 South Wacker Drive, Suite 3000

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/866,979

; FILING DATE: 19920410

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5532347nan, Kevin E

; REGISTRATION NUMBER: 35,303

; REFERENCE/DOCKET NUMBER: 92,154

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-715-1000

; TELEFAX: 312-715-1234

; TELEX: 910-221-5317

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1633 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 462..1415

; FEATURE:

; NAME/KEY: 5'UTR

; LOCATION: 1..461

; FEATURE:

; NAME/KEY: 3'UTR

; LOCATION: 1416..1633

US-07-866-979-5

Alignment Scores:

Pred. No.: 1.07 Length: 1633

Score: 89.50 Matches: 49

Percent Similarity: 38.25% Conservative: 21

Best Local Similarity: 26.78% Mismatches: 62

Query Match: 8.79% Indels: 51

DB: 1 Gaps: 8

US-10-030-937-9 (1-193) x US-07-866-979-5 (1-1633)

QY 26 LysLysProSerGlnLeu-----SerSer 33

Db 595 AAGAGCCCGTCAGAGATGACACCTCCAGGCACCGGGCTCCTGTCTGTGGTGGCAGCAGC 536

QY 34 PheSerTrpAspAsnCys-----PheGluGlyLysAspProAlaValIleArgSerLeu 51

Db 535 CCCAGCTGGGGGATGGCTGTGGGGGTGGAGTTGAGGGAGCCC-----AGAAAGTCTT 485

QY 52 ThrLeuGluProAspProIleValValProGlyAsnValThrLeuSerValValGlySer 71

Db 484 CTCTGGGATCCCTGCACAGCCATAGTCTCTGTCCAGGAAGCAGGAAGGAGTCTGTGGAGGC 425

QY 72 ThrSerValProLeuSerSerProLeuLysValAspLeuValLeuGluLysGluValAla 91

Db 424 CTCAGGTCCCCACAGTTCTTCCCTCCAGGTGTCTGTCTAGTTTCATGTGTGCTGCCAGG 365

QY 92 GlyLeuTrpIleLysIleProCysThrAspTyrIleGlySerCysThrPheGluHisPhe 111

Db 364 GGGCCTTGGGTGCC---CCATGC----- 344

QY 112 CysAspValLeuAspMet-LeuIleProThrGlyGluPro-----CysPro--GluPro 128

Db 343 -----CTGCCTCCTTCCATCTGGGCACCCCGACAGATCTGCCCTCACACCT 299

QY 129 LeuArgThrTyr---GlyLeuProCysHisCysProPheLysGluGlyThrTyr----- 145

Db 298 CTCCTGGCTGGACAGGTGAGCCAGGCATGGCCAGCCAGTCCAGACACCTCTCTGGCAT 239

QY 146 -----SerLeuProLysSerGluPheAlaValProAspLeuGlu 158

Db 238 CAACCGCCTGGGCTCAGGGATCTCACAAACCAAGCCTGGTCTCAGTCTCCTCCTGCCT 179

QY 159 LeuProSerTrpLeu-ThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGl 178

Db 178 CTTCCCTGGTGGCTGCTGTCTCAGGTTCCAGGACATTTCGACACCTCTGGACCGTCTGG 119

QY 178 Y 178

Db 118 C 118

RESULT 13

US-08-466-906B-5/c

; Sequence 5, Application US/08466906B

; Patent No. 5849871

; GENERAL INFORMATION:

; APPLICANT: Cone, Roger D

; APPLICANT: Mountjoy, Kathleen G

; TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor

; TITLE OF INVENTION: and Uses

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff

; STREET: 300 South Wacker Drive

; CITY: Chicago

; STATE: IL

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/466,906B

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5849871nan, Kevin E

; REGISTRATION NUMBER: 35,303

; REFERENCE/DOCKET NUMBER: 92,154-H

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-913-0001

; TELEFAX: 312-913-0002

; TELEX:

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1633 base pairs

; TYPE: nucleic acid

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..461
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 462..1415
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1416..1633
US-08-466-906B-5

Alignment Scores:
Pred. No.: 1.07 Length: 1633
Score: 89.50 Matches: 49
Percent Similarity: 38.25% Conservative: 21
Best Local Similarity: 26.78% Mismatches: 62
Query Match: 8.79% Indels: 51
DB: 2 Gaps: 8

US-10-030-937-9 (1-193) x US-08-466-906B-5 (1-1633)

Qy 26 LysLysProSerGlnLeu-----SerSer 33
Db 595 AAGAGCCCGTCAGAGATGGACACCTCCAGGCACCGGGCTCCTGTCTGTTGGCAGCCAGC 536
Qy 34 PheSerTrpAspAsnCys-----PheGluGlyLysAspProAlaValIleArgSerLeu 51
Db 535 CCCAGCTGGGGATGGCTGTGGGGTGGAGTTGAGGGAGCCC-----AGAAGTCTT 485
Qy 52 ThrLeuGluProAspProIleValProGlyAsnValThrLeuSerValValGlySer 71
Db 484 CTCTGGGATCCCTGCACAGCCATAGTCTGTCTCCAGGACGAGGAGAGTCTGTTGGAGGC 425
Qy 72 ThrSerValProLeuSerSerProLeuLysValAspLeuValLeuGluLysGluValAla 91
Db 424 CTCCAGGTCCCCACAGTTCTTCCCTCCAGGTGTCTGCTTAGTTTCATGTTGTCGCCAGG 365
Qy 92 GlyLeuTrpIleLysIleProCysThrAspTyrIleGlySerCysThrPheGluHisPhe 111
Db 364 GGGCCTTGGGTGCC----CCATGC-----344
Qy 112 CysAspValLeuAspMet-LeuIleProThrGlyGluPro-----CysPro--GluPro 128
Db 343 -----CTGCCCTCCTTCCATCTGGGCACCCCCAGATCTGCCCTCACACCCCT 299
Qy 129 LeuArgThrTyr---GlyLeuProCysHisCysProPheLysGluGlyThrTyr----- 145
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Qy 146 -----SerLeuProLysSerGluPheAlaValProAspLeuGlu 158
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US-08-706-281A-5/c
; Sequence 5, Application US/08706281A
; Patent No. 6100048
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; APPLICANT: Fan, Wei
; APPLICANT: Boston, Bruce A
; APPLICANT: Kesterton, Robert A
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; APPLICANT: Lu, Dongsi
; APPLICANT: Chen, Wenbiao
; TITLE OF INVENTION: Methods and Reagents for Discovering and
; TITLE OF INVENTION: Using Mammalian Melanocortin Receptor Agonists and Antagonists
; TITLE OF INVENTION: To Modulate Feeding Behavior in Animals
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,281A
; FILING DATE: 04-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6100048nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 96,886
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1633 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..461
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 462..1415
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; NAME/KEY: 3'UTR
; LOCATION: 1416..1633
US-08-706-281A-5

Alignment Scores:
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US-10-030-937-9 (1-193) x US-08-706-281A-5 (1-1633)

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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(without alignments)
1048.964 Million cell updates/sec

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Perfect score: 1018
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Searched: 7277826 seqs, 3233139505 residues

Total number of hits satisfying chosen parameters: 14555652

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1005	98.7	2436	9	US-09-954-531-380	Sequence 380, Appl
2	1005	98.7	2436	10	US-09-525-978B-81	Sequence 81, Appl
3	1005	98.7	2436	21	US-10-843-641A-1447	Sequence 1447, Ap
4	1005	98.7	2478	17	US-10-170-385-390	Sequence 390, App
5	1000	98.2	953	20	US-10-723-860-528	Sequence 528, App
6	1000	98.2	1935	10	US-09-971-392-102	Sequence 102, App
7	1000	98.2	2384	9	US-09-822-849A-53	Sequence 53, Appl
8	1000	98.2	3988	20	US-10-723-860-5187	Sequence 5187, Ap
9	740.5	72.7	1983	17	US-10-388-934-167	Sequence 167, App
10	424	41.7	577	17	US-10-264-049-436	Sequence 436, App
11	367.5	36.1	596	22	US-10-972-079-7219	Sequence 7219, Ap
12	367.5	36.1	599	22	US-10-972-079-7218	Sequence 7218, Ap
c 13	354	34.8	475	9	US-09-864-761-1518	Sequence 1518, Ap
14	333	32.7	448	11	US-09-969-034-4215	Sequence 4215, Ap
15	272	26.7	546	13	US-10-027-632-207798	Sequence 207798,
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18	272	26.7	546	13	US-10-027-632-207801	Sequence 207801,
19	272	26.7	546	17	US-10-027-632-207798	Sequence 207798,
20	272	26.7	546	17	US-10-027-632-207799	Sequence 207799,
21	272	26.7	546	17	US-10-027-632-207800	Sequence 207800,
22	272	26.7	546	17	US-10-027-632-207801	Sequence 207801,
c 23	270	26.5	145	9	US-09-864-761-18277	Sequence 18277, A
c 24	262.5	25.8	250000	16	US-10-225-810-26	Sequence 26, Appl
c 25	254	25.0	857	13	US-10-027-632-164063	Sequence 164063,
c 26	254	25.0	857	13	US-10-027-632-164064	Sequence 164064,
c 27	254	25.0	857	13	US-10-027-632-164065	Sequence 164065,
c 28	254	25.0	857	17	US-10-027-632-164063	Sequence 164063,
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31	221	21.7	380	10	US-09-764-891-2290	Sequence 2290, Ap
32	145	14.2	593	13	US-10-027-632-277778	Sequence 277778,
c 33	145	14.2	593	17	US-10-027-632-277778	Sequence 277778,
c 34	103	10.1	4821	20	US-10-425-115-178335	Sequence 178335,
35	98.5	9.7	819	20	US-10-425-115-112475	Sequence 112475,
36	97.5	9.6	20966	9	US-09-776-976-7	Sequence 7, Appli
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44	95.5	9.4	638	21	US-10-487-901-3700	Sequence 3700, Ap
45	95.5	9.4	670	21	US-10-487-901-3699	Sequence 3699, Ap

ALIGNMENTS

RESULT 1
US-09-954-531-380
; Sequence 380, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034

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; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 380
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-380

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Pred. No.:      6,47e-117      Length:      2436
Score:          1005.00      Matches:      191
Percent Similarity: 98.96%      Conservative: 0
Best Local Similarity: 98.96%      Mismatches: 2
Query Match:    98.72%      Indels:      0
DB:              9      Gaps:          0

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Qy      41 GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVal 60
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Qy      121 ThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPhe 140
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Qy      181 LeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle 193
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RESULT 2
US-09-525-978B-81
; Sequence 81, Application US/09525978B
; Publication No. US2003004972A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Caras, Ingrid W.
; APPLICANT: Hevezi, Peter
; APPLICANT: Wilson, Keith
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING MACROPHAGE DEVELOPMENT

; TITLE OF INVENTION: RELATED DISORDERS, COMPOSITIONS, AND METHODS OF
; TITLE OF INVENTION: SCREENING FOR MACROPHAGE DEVELOPMENT MODULATORS
; FILE REFERENCE: A-67413-1/DJB/JJD
; CURRENT APPLICATION NUMBER: US/09/525,978B
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: USSN 60/124,530
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-525-978B-81

Alignment Scores:
Pred. No.:      6,47e-117      Length:      2436
Score:          1005.00      Matches:      191
Percent Similarity: 98.96%      Conservative: 0
Best Local Similarity: 98.96%      Mismatches: 2
Query Match:    98.72%      Indels:      0
DB:              10      Gaps:          0

US-10-030-937-9 (1-193) x US-09-525-978B-81 (1-2436)

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Qy      21 AlaGlnAlaHisLeuLysLysProSerGlnLeuSerSerPheSerTrpAspAsnCysPhe 40
Db      119 GCGCAAGCCACCTGAAAAGCCATCCAGCTCAGTAGCTTTTCTGGGATAACTGTGAT 178
Qy      41 GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVal 60
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Db      299 AAGGTGGATTAGTTTGGAGAAGGAGGTGGCTGGCTCTGGATCAAGATCCCATGCGACA 358
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Qy      161 SerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerGlyLysArg 180
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RESULT 3
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; Sequence 1447, Application US/10843641A
; Publication No. US2005006445A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; APPLICANT: Hevezi, Peter
; APPLICANT: Wilson, Keith
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
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; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1447
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-1447

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Best Local Similarity: 98.96%      Mismatches:  2
Query Match:    98.72%          Indels:       0
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Db      119 GCGCAAGCCACCTGAAAAGCCATCCAGCTCAGTAGCTTTTCTGGGATAACTGTGAT 178
QY      41 GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVal 60
Db      179 GAAGGGAGGACCCCTGCGGTGATCAGAGCCCTGACTCTGGAGCCCTGACCCCATCGTCGT 238
QY      61 ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLeu 80
Db      239 CCTGGAAATGTGACCCCTCAGTGTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 298
QY      81 LysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCysThr 100
Db      299 AAGGTGGATTAGTTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 358
QY      101 AspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIlePro 120
Db      359 GACTACATTTGGCAGCTGTACCTTTTGAAACACTTCTGTGATGTGCTTGGATCAAGATCCCA 418
QY      121 ThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPhe 140
Db      419 ACTGGGAGGCCCTGCCAGAGGCCCTGCCGTACCTATGGGCTTCTTGGCCACTGTCCCTTC 478
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Db      479 AAAGAGGAACCTACTCACTGCCCCAAGAGCGAATTCTGTTGTGCTGACCTGGAGCTGCC 538
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QY      181 LeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle 193
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RESULT 4
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; Sequence 390, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390
; LENGTH: 2478
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-170-385-390
```

```
Alignment Scores:
Pred. No.:      6.63e-117      Length:      2478
Score:          1005.00        Matches:      191
Percent Similarity: 98.96%      Conservative: 0
Best Local Similarity: 98.96%      Mismatches:  2
Query Match:    98.72%          Indels:       0
DB:             17             Gaps:         0

US-10-030-937-9 (1-193) x US-10-170-385-390 (1-2478)

QY      1 MetGlnSerLeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrPro 20
Db      96 ATGCAGTCCCTGATGCAGGCTCCCTCTGTATCGCCCTGGGCTTGCTTCTCGGACCCCT 155
QY      21 AlaGlnAlaHisLeuLysProSerGlnLeuSerSerPheSerTrpAspAsnCysPhe 40
Db      156 GCGCAAGCCACCTGAAAAGCCATCCAGCTCAGTAGCTTTTCTGGGATAACTGTGAT 215
QY      41 GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVal 60
Db      216 GAAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 275
QY      61 ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLeu 80
Db      276 CCTGGAAATGTGACCCCTCAGTGTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 335
QY      81 LysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCysThr 100
Db      336 AAGGTGGATTAGTTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 395
QY      101 AspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIlePro 120
Db      396 GACTACATTTGGCAGCTGTACCTTTTGAAACACTTCTGTGATGTGCTTGGATCAAGATCCCA 455
```

[illegible]

Db 402 GACTACATTGGCAGCTGTACCTTTGAACACTTCTGTGATGTGCTTGACATGTTAATTCCT 461
QY 121 ThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPhe 140
Db 462 ACTGGGAGCCCTGCCAGAGCCCTGGTACCTATGGGCTTCTTGCCACTGTCCCTTC 521
QY 141 LysGluGlyThrTyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 160
Db 522 AAAGAAGGAACCTACTCACTGCCCAAGAGCGAATTGTTGCTTGACCTGGAGTGGCC 581
QY 161 SerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysArg 180
Db 582 AGTTGGCTCACCACCGGAACCTACCGCATAGAGCGTCTCTGAGCAGCAGTGGGAAGCGT 641
QY 181 LeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle 193
Db 642 CTGGGCTGCATCAAGATCGTGCCTCTCTAAAGGGGCATA 680

RESULT 7

US-09-822-849A-53
; Sequence 53, Application US/09822849A
; Patent No. US20020045170A1
; GENERAL INFORMATION:

; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.

; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6403

; CURRENT APPLICATION NUMBER: US/09/822,849A

; CURRENT FILING DATE: 2001-09-04

; PRIOR APPLICATION NUMBER: 60/195,582

; PRIOR FILING DATE: 2000-04-06

; NUMBER OF SEQ ID NOS: 598

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 53

; LENGTH: 2384

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-822-849A-53

Alignment Scores:
Pred. No.: 2,72e-116 Length: 2384
Score: 1000.00 Matches: 190
Percent Similarity: 98.45% Conservative: 0
Best Local Similarity: 98.45% Mismatches: 3
Query Match: 98.23% Indels: 0
DB: 9 Gaps: 0

US-10-030-937-9 (1-193) x US-09-822-849A-53 (1-2384)

QY 1 MetGlnSerLeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrPro 20
Db 13 ATGCAGTCCCTGTATGATGAGGCTCCCTCTCTGATCGCCCTGGGCTTGTCTCGCGGCCCT 72
QY 21 AlaGlnAlaHisLeuLysLysProSerGlnLeuSerSerPheSerTrpAspAsnCysPhe 40
Db 73 GCGCAAGCCACCTGAAAGAGCCATCCAGCTCAGTAGCTTTTCTGGGATAACTGTGAT 132
QY 41 GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVal 60
Db 133 GAAGGGAAGGACCTCGCGGTGATCAGAAGCCTGACTCTGGAGCCTGACCCCATCGTCGTT 192
QY 61 ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLeu 80
Db 193 CCTGGAATGTGACCCCTCAGTGTCTGGGCAGCACCAAGTGTCCCTCCTGAGTTCTCTCTG 252

QY 81 LysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCysThr 100
Db 253 AAGGTGGATTTAGTTTGGAGAAGGAGGTGGTGGCCTCTGGATCAAGATCCCATGCACA 312
QY 101 AspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIlePro 120
Db 313 GACTACATTGGCAGCTGTACCTTTGAACACTTCTGTGATGTGCTTGACATGTTAATTCCT 372
QY 121 ThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPhe 140
Db 373 ACTGGGAGCCCTGCCAGAGCCCTGCGTACTATATGGGCTTCTTGCCACTGTCCCTTC 432
QY 141 LysGluGlyThrTyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 160
Db 433 AAAGAAGGAACCTACTCACTGCCCAAGAGCGAATTGTTGCTTGACCTGGAGTGGCC 492
QY 161 SerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysArg 180
Db 493 AGTTGGCTCACCACCGGAACCTACCGCATAGAGCGTCTCTGAGCAGCAGTGGGAAGCGT 552

RESULT 8

US-10-723-860-5187

; Sequence 5187, Application US/10723860

; Publication No. US20040253606A1

; GENERAL INFORMATION:

; APPLICANT: Aziz, Natasha

; APPLICANT: Ginsburg, Wendy M.

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01

; CURRENT APPLICATION NUMBER: US/10/723,860

; CURRENT FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: 60/429,739

; PRIOR FILING DATE: 2002-11-26

; NUMBER OF SEQ ID NOS: 8393

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 5187

; LENGTH: 3988

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (2864)..(2894)

; OTHER INFORMATION: n is a, c, g, or t

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (3472)..(3486)

; OTHER INFORMATION: n is a, c, g, or t

US-10-723-860-5187

Alignment Scores:
Pred. No.: 5.69e-116 Length: 3988
Score: 1000.00 Matches: 190
Percent Similarity: 98.45% Conservative: 0
Best Local Similarity: 98.45% Mismatches: 3
Query Match: 98.23% Indels: 0
DB: 20 Gaps: 0

US-10-030-937-9 (1-193) x US-10-723-860-5187 (1-3988)

QY 1 MetGlnSerLeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrPro 20
Db 96 ATGCAGTCCCTGTATGATGAGGCTCCCTCTCTGATCGCCCTGGGCTTGTCTTCGCGGCCCT 155
QY 21 AlaGlnAlaHisLeuLysLysProSerGlnLeuSerSerPheSerTrpAspAsnCysPhe 40
Db 156 GCGCAAGCCACCTGAAAGAGCCATCCAGCTCAGTAGCTTTTCTGGGATAACTGTGAT 215

Qy	41	GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVal	60
Db	216	GAAGGGAAAGGACCCCTGCGGTGATCAGAAGCCCTGACTCTGGAGCCTGACCCCACATCGTCGT	275
Qy	61	ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLeu	80
Db	276	CCTGGAAAATGTGACCCTCAGTGTCTGGGGCAGCACCAAGTGTCCTCCCTGAGTTCTCCCTCTG	335
Qy	81	LysValAspLeuValLeuGluLysGluValAlaAlaGlyLeuTrpIleLysIleProCysThr	100
Db	336	AAGTGGATTATAGTTTGGAGAAGGAGGTGGCTGGCTCTGGATCAAGATCCCATGCACA	395
Qy	101	AspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIlePro	120
Db	396	GACTACATTGGCAGCTGTACCTTTGAACACTTCTCTGTGATGTGCTTGACATGTTAATTCCT	455
Qy	121	ThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPhe	140
Db	456	ACTGGGGAGCCCTGCCCAGAGCCCTGCGTACCTATGGGCTTCCTTGCCACTGTCCCTTC.	515
Qy	141	LysGluGlyThrTyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro	160
Db	516	AAAGAAGGAACCTACTCAGTCCCAAGAGCGAATTCGTTGTGCCTGACCTGGAGCTGCC	575
Qy	161	SerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysArg	180
Db	576	AGTTGGCTCACCAACGGGAACCTACCGCATAGAGAGCGCTCTGTAGCAGCAGTGGGAAGCGT	635
Qy	181	LeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle	193
Db	636	CTGGSGCTGCATCAAGATCGCTGCCTCTCTAAAGGGCATA	674

RESULT 9

US-10-388-934-167
; Sequence 167, Application US/10388934
; Publication No. US20040005547A1
; GENERAL INFORMATION:
; APPLICANT: Boess, Franziska
; APPLICANT: Suter-Dick, Laura
; APPLICANT: Wolf, Detlef
; TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
; FILE REFERENCE: 21199
; CURRENT APPLICATION NUMBER: US/10/388,934
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 02005336.9
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 02015657.6
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 862
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
; LENGTH: 1983
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-388-934-167

Qy	34	PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArgSerLeuThrLeu	53
Db	129	TTCTCCTGGGATAACTGTGATGAAGGAAAGACCCCTGCAGTGATCAAAGACCTCAGGCTC	188
Qy	54	GluProAspProIleValValProGlyAsnValThrLeuSerValValGlySerThrSer	73
Db	189	CAACCTGACCCCAATTGTCGTCCTGGAGATGTGATCGTCAGTGCTGAGGGCAAGACCAGC	248
Qy	74	ValProLeuSerSerProLeuLysValAspLeuValLeuGluLysGluValAlaGlyLeu	93
Db	249	ATTCCCTCACTTCTCCTCAGAAGGTGGAGCTCACCGTGGAGAAGGAAGTGGCTGGGCTTC	308
Qy	94	TrpIleLysIleProCysThrAspTyrIleGlySerCysThrPheGluHisPheCysAsp	113
Db	309	TGGGTCAAGATCCCTTGCGTAGAACAGCTAGGAAGCTGTACCTATGAGAAATGTCCTGAC	368
Qy	114	ValLeuAspMetLeuIleProThrGlyGluProCysProGluProLeuArgThrTyrGly	133
Db	369	CTGATAGACCAATACATCCCCCTGGAGAGACCTGCCAGAGCCGCTGCACACCTACGGG	428
Qy	134	LeuProCysHisCysProPheLysGluGlyThrTyrSerLeuProLysSerGluPheAla	153
Db	429	CTGCCCTGCCATTGTCCCTTCAAGGAAGGCACCTACTCACTGCGCTTCGAGCAACTTCACA	488
Qy	154	ValProAspLeuGluLeuProSerTrpLeuThrThrGlyAsnTyrArgIleGluSerVal	173
Db	489	GTGCCTGATCTGGAGCTTCCAAGCTGGCTAAGCAGCGGGCAACTACCGCATCCAGAGCATC	548
Qy	174	LeuSerSerSerGlyLysArgLeuGlyCysIleLysIleAlaAlaSerLeuLysGly	192
Db	549	TTGAGCAGCGGTGAAAGCGCTGGCTGTCATCAAGATTGCCGCTCTCTCAAGGGC	605

RESULT 10

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US-10-264-049-436
; Sequence 436, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Protei
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 436
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (536)..(536)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (552)..(552)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (561)..(561)
; OTHER INFORMATION: n equals a,t,g, or c
; US-10-264-049-436

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Alignment scores:		
Pred. No.:	8.58e-44	577
Score:	424.00	96
Percent Similarity:	67.60%	25
Best Local Similarity:	53.63%	48
Query Match:	41.65%	14
Matches:		
Conservative:		
Mismatches:		
Indels:		

DB: 17 Gaps: 3

US-10-030-937-9 (1-193) x US-10-264-049-436 (1-577)

QY 1 MetGlnSerLeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAla----- 18

Db 37 ATGATGCTGAAGATGAGGCTCTCTTGATGGC-CTTGGGCTGCTTCTCGCGGCCCT 95

QY 19 -----ThrProAlaGlnAlaHisLeuLysLysProSerGlnLeuSerSer 33

Db 96 GCGGCCACGCACACGTCCTCCCGCCCGCCCGGCGGTAACCCGCCACCCAGGTAATTAGC 155

QY 34 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArgSerLeuThrLeu 53

Db 156 TTTTCTGGGAGAACTGCCATGAAGGAAGGCCCTGTGTCTGCTCAAAAGCATGACTCTG 215

QY 54 GluProAspProIleValValProGlyAsnValThrLeuSerValValGlySerThrSer 73

Db 216 GAACCTGACCCCATTCCTATCTGGGAATGTACTATCAGCGCCGAGCTCCAGGTCCGT 275

QY 74 ValProLeuSerSerProLeuLysValAspLeuValLeuGluLysGluValAlaGlyLeu 93

Db 276 GTCCCCCTCAGCAGTCTCAGAGGTGGAATTAATTATAGAGAAAGTGCCCAATTTC 335

QY 94 TrpIleLysIleProCysThrAspTyrIleGlySerCysThrPheGluHisPheCysAsp 113

Db 336 TGGATCAAAAGTTCCATGTATGAGCCATGTT---CGTTGCATCTTTGAAGACATYTGCAA 392

QY 114 ValLeuAspMetLeuIleProThrGlyGluProCysProGluProLeuArgThrTyrGly 133

Db 393 ATATTAGACTTTTAAATCCCTCCCTGGACAGSCCTGSCAGAGCCCTGCATACCTATGGG 452

QY 134 LeuProCysHisCysProPheLysGluGlyThrTyrSerLeuProLys---SerGluPhe 152

Db 453 CTTCCCTGCAC-TGTSCCTCAAGCA-GGCACCTACTCAATGCCCCAAAGACTCAAGTTAC 510

QY 153 AlaValProAspLeuGluLeuProSerTrpLeuThrThr-GlyAsnTyrArgile 170

Db 511 CC-TGCCAAACACGGACCTGCCCGGNTGTATCACCTCCGGNTCTACCGNATT 564

RESULT 11

US-10-972-079-7219

; Sequence 7219, Application US/10972079

; Publication No. US20050153317A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: ROSENFELD, David

; APPLICANT: KERR, Richard

; APPLICANT: BATES, Stephen

; APPLICANT: HOLM, Tom

; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF

; TITLE OF INVENTION: LIVESTOCK

; FILE REFERENCE: MM1110-2

; CURRENT APPLICATION NUMBER: US/10/972,079

; CURRENT FILING DATE: 2004-10-22

; PRIOR APPLICATION NUMBER: US 60/514,333

; PRIOR FILING DATE: 2003-10-24

; NUMBER OF SEQ ID NOS: 96631

; SOFTWARE: PatentIN version 3.1

; SEQ ID NO 7219

; LENGTH: 596

; TYPE: DNA

; ORGANISM: Chicken 19866894191999_2

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(32)

; OTHER INFORMATION: n is any nucleotide

US-10-972-079-7219

Alignment Scores:

Pred. No.: 1.42e-36 Length: 596

Score: 367.50 Matches: 70

Percent Similarity: 62.84% Conservative: 23

Best Local Similarity: 47.30% Mismatches: 30

Query Match: 36.10% Indels: 26

DB: 22 Gaps: 2

US-10-030-937-9 (1-193) x US-10-972-079-7219 (1-596)

QY 69 ValGlySerThrSerValProLeuSerSerPro---LeuLysValAspLeuValLeuGlu 87

Db 51 GTCGGGAGGGAGGGCTGGGTGCTCAGTGTCTTCTTACAGGGGTGTGGTGGTGAG 110

QY 88 LysGluValAlaGlyLeuTrpIleLysIleProCysThrAspTyrIleGlySerCysThr 107

Db 111 AAGGCCTTGGGTGACCTCTGGATCCAGCTGCCCTGCATCGACCAAGCTGGCAGCTGCACC 170

QY 108 PheGluHisPheCysAspValLeuAspMetLeuIleProThrGlyGluProCysProGlu 127

Db 171 TATGATGATGTGTCAACATCTCGACAACCTCATCCACCCGCGCACRCCCTGCCCGGAG 230

QY 128 ProLeuArgThrTyrGlyLeuProCysHisCysProPheLysGluGlyThr----- 144

Db 231 CCGCTGCTCACCTACGCGCATCCCTGCCACTGCCACTGCCCTTCAAGGC-GGTACGTCCCAAC 289

QY 144 ----- 144

Db 290 CGGCTGCCCTYGGTGTGTGGGGTCGGTGTGGCTCACGCGAGCCCTCTCTCTGAGGGC 349

QY 145 ---TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuProSerTrpLeu 163

Db 350 TCCTACTCACTGCCCGCCAGCACTTCGCCCTGCCCGACGTCAGCTGCCCTCTCTGATG 409

QY 164 ThrThrGlyAsnTyrArgileGluSerValLeuSerSerSerGlyLysArgLeuGlyCys 183

Db 410 ACCAAGGCAACTACCGTGTGCGAGTGTGTCGTCAGCAACAAGGGGCGAGGCTCGCCTGC 469

QY 184 IleLysIleAlaAlaSerLeuLys 191

Db 470 GTCAAGCTGGGCTTCTCTTGCAG 493

RESULT 12

US-10-972-079-7218

; Sequence 7218, Application US/10972079

; Publication No. US20050153317A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: ROSENFELD, David

; APPLICANT: KERR, Richard

; APPLICANT: BATES, Stephen

; APPLICANT: HOLM, Tom

; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF

; TITLE OF INVENTION: LIVESTOCK

; FILE REFERENCE: MM1110-2

; CURRENT APPLICATION NUMBER: US/10/972,079

; CURRENT FILING DATE: 2004-10-22

; PRIOR APPLICATION NUMBER: US 60/514,333

; PRIOR FILING DATE: 2003-10-24

; NUMBER OF SEQ ID NOS: 96631

; SOFTWARE: PatentIN version 3.1

; SEQ ID NO 7218

; LENGTH: 599

; TYPE: DNA

; ORGANISM: Chicken 19866894191999_1

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(114)

; OTHER INFORMATION: n is any nucleotide

US-10-972-079-7218

Alignment Scores:

Pred. No.: 1.43e-36 Length: 599

Score: 367.50 Matches: 70

Percent Similarity: 62.84% Conservative: 23


```
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; TITLE OF INVENTION: Expressed in Cancer Tissue
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4215
; LENGTH: 448
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 241, 277, 288, 295, 299, 300, 304, 310, 316, 343, 346, 356,
; LOCATION: 364, 370, 396, 397, 406, 410, 415, 424, 437
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-4215

Alignment Scores:
Pred. No.:      2.34e-32      Length:      448
Score:          333.00      Matches:      62
Percent Similarity: 98.41%      Conservative: 0
Best Local Similarity: 98.41%      Mismatches: 1
Query Match:      32.71%      Indels:      0
DB:              11          Gaps:      0

US-10-030-937-9 (1-193) x US-09-969-034-4215 (1-448)

QY      131 ThrTyrGlyLeuProCysHisCysProPheLysGluGlyThrTyrSerLeuProLysSer 150
      |||
Db      1 ACCTATGGGCTTCCTTGGCCACTGTCCCTCAAAGAGGAACCTACTCCTGCCCAAGAGC 60

QY      151 GluPheAlaValProAspLeuGluLeuProSerTrpLeuThrThrGlyAsnTyrArgIle 170
      |||
Db      61 GAATTCGTGTGCTGACCTGGAGCTGCCAGTTGGCTCACCACCGGAACCTACCGCATA 120

QY      171 GluSerValLeuSerSerGlyLysArgLeuGlyCysIleLysIleAlaAlaSerLeu 190
      |||
Db      121 GAGAGCTCCTGAGCAGCAGTGGGAGCGTCTGGGCTGCATCAAGATCGCTGCTCTCTA 180

QY      191 LysGlyIle 193
      |||
Db      181 AAGGGCATA 189

RESULT 15
US-10-027-632-207798
; Sequence 207798, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 10827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 207798
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-207798

Alignment Scores:
Pred. No.:      1.84e-24      Length:      546
Score:          272.00      Matches:      57
Percent Similarity: 86.76%      Conservative: 2
Best Local Similarity: 83.82%      Mismatches: 7
Query Match:      26.72%      Indels:      2
DB:              13          Gaps:      1

US-10-030-937-9 (1-193) x US-10-027-632-207798 (1-546)

QY      27 LysProSerGlnLeuSerSerPheSerTrpAspAsnCysPheGluGlyLysAspProAla 46
      ::|||
Db      255 CAGCCATCCCAGCTCAGTAGCTTTCTCTGGGATACTGTGATGAAGGAAGGACCCCTGCG 314

QY      47 ValIleArgSerLeuThrLeuGluProAspProIleValValProGlyAsnValThrLeu 66
      |||
Db      315 GTGATCAGAAGCCTGACTCTGGAGCCTGACCCCATCRTCCTCTGGAAATGTGACCCCTC 374

QY      67 SerValValGlySerThrSerValProLeuSerSerProLeuLysValAspLeuValLeu 86
      |||
Db      375 AGTGTCTRTGGGCAGCACCACTGTCCCCCTGAGTTCCTCTCTGAAGGTGAGCCCTGGGGGTG 434

QY      87 -----GluLysGluValAlaGly 92
      |||
Db      435 GGTGGAGAAGGGGAGGTGCGAGGG 458

Search completed: July 27, 2005, 22:48:00
Job time : 1193.74 secs
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OM protein - protein search, using sw model

Run on: July 27, 2005, 18:58:36 ; Search time 36.8844 Seconds
(without alignments)
390.606 Million cell updates/sec

Title: US-10-030-937-9
Perfect score: 193
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	112	58.0	193	4	US-09-183-841-1
3	10	5.2	362	4	US-09-902-540-12082
4	9	4.7	262	3	US-08-961-083-98
5	9	4.7	262	4	US-09-536-784-98
6	9	4.7	270	3	US-08-961-083-206
7	9	4.7	270	4	US-09-536-784-206
8	9	4.7	291	4	US-09-583-110-4201
9	9	4.7	328	4	US-09-107-433-3318
10	8	4.1	390	4	US-09-949-016-6952
11	8	4.1	444	4	US-09-252-991A-20496
12	8	4.1	563	4	US-09-252-991A-23790
13	8	4.1	769	3	US-09-320-878-12
14	8	4.1	769	4	US-09-141-908-10
15	8	4.1	769	4	US-09-657-440-12
16	8	4.1	809	3	US-09-105-537-24
17	8	4.1	3782	3	US-09-105-537-4
18	7	3.6	85	4	US-09-270-767-32129
19	7	3.6	85	4	US-09-270-767-47346
20	7	3.6	96	3	US-08-936-165A-401
21	7	3.6	103	4	US-09-270-767-33345
22	7	3.6	103	4	US-09-270-767-48562
23	7	3.6	115	4	US-09-746-801A-47
24	7	3.6	153	3	US-09-199-637A-213
25	7	3.6	168	4	US-09-902-540-16420
26	7	3.6	170	4	US-09-205-258-1011
27	7	3.6	213	4	US-09-902-540-13301

28	7	3.6	267	4	US-09-489-039A-12889	Sequence 12889, A
29	7	3.6	269	4	US-09-543-681A-6475	Sequence 6475, Ap
30	7	3.6	285	1	US-08-149-809-24	Sequence 24, Appl
31	7	3.6	287	4	US-09-540-236-2879	Sequence 2879, Ap
32	7	3.6	301	4	US-09-902-540-11985	Sequence 11985, A
33	7	3.6	315	4	US-09-252-991A-31850	Sequence 31850, A
34	7	3.6	324	4	US-09-489-039A-7803	Sequence 7803, Ap
35	7	3.6	325	2	US-08-828-242-4	Sequence 4, Appli
36	7	3.6	325	3	US-09-206-499-4	Sequence 4, Appli
37	7	3.6	331	2	US-08-828-242-3	Sequence 3, Appli
38	7	3.6	331	2	US-08-910-927B-5	Sequence 5, Appli
39	7	3.6	331	3	US-09-206-499-3	Sequence 3, Appli
40	7	3.6	331	3	US-09-270-270-5	Sequence 5, Appli
41	7	3.6	331	4	US-09-961-403-11	Sequence 11, Appl
42	7	3.6	348	4	US-09-949-016-9513	Sequence 9513, Ap
43	7	3.6	355	4	US-09-580-929-5	Sequence 5, Appli
44	7	3.6	364	4	US-09-205-258-1008	Sequence 1008, Ap
45	7	3.6	369	4	US-09-489-039A-8053	Sequence 8053, Ap

ALIGNMENTS

RESULT 1
US-09-183-841-2
; Sequence 2, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanz0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: His tag at residues 1 to 17
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence of GM2 protein using His6 tag
US-09-183-841-2

Query Match	58.0%;	Score 112;	DB 4;	Length 178;
Best Local Similarity	100.0%;	Pred. No. 3.1e-102;		
Matches 112;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	41	EGKDPAVIRSLTLEPDPPIVPGNVTL	SVGSTSVPLSSPLKVDLVLEKEVAGLWIKIPCT	100
Db	26	EGKDPAVIRSLTLEPDPPIVPGNVTL	SVGSTSVPLSSPLKVDLVLEKEVAGLWIKIPCT	85
QY	101	DYIGSCTFEHFCDVLDMLIPTGECPEPLRTYGLPCHCPFKEGTYSLPKSEF	152	
Db	86	DYIGSCTFEHFCDVLDMLIPTGECPEPLRTYGLPCHCPFKEGTYSLPKSEF	137	

RESULT 2
US-09-183-841-1
; Sequence 1, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanz0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 193


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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 98:
US-09-536-784-98

Query Match      4.7%; Score 9; DB 4; Length 262;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      66 LSVVGSTSV 74
      |||||
Db      155 LSVVGSTSV 163

RESULT 6
US-08-961-083-206
; Sequence 206, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-961-083-206

Query Match      4.7%; Score 9; DB 3; Length 270;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      66 LSVVGSTSV 74
      |||||
Db      163 LSVVGSTSV 171

RESULT 7
US-09-536-784-206
; Sequence 206, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-09-536-784-206

Query Match      4.7%; Score 9; DB 4; Length 270;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      66 LSVVGSTSV 74
      |||||
Db      163 LSVVGSTSV 171

RESULT 8
US-09-583-110-4201
; Sequence 4201, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4201
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4201

Query Match      4.7%; Score 9; DB 4; Length 291;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 66 LSVVGSTSV 74
Db 184 LSVVGSTSV 192

RESULT 9
US-09-107-433-3318
; Sequence 3318, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3318:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...328
; SEQUENCE DESCRIPTION: SEQ ID NO: 3318:
US-09-107-433-3318

Query Match 4.7%; Score 9; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 LSVVGSTSV 74
Db 221 LSVVGSTSV 229

RESULT 10
US-09-949-016-6952
; Sequence 6952, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6952
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6952

Query Match 4.1%; Score 8; DB 4; Length 390;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 LEKEVAGL 93
Db 277 LEKEVAGL 284

RESULT 11
US-09-252-991A-20496
; Sequence 20496, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20496
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (31)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-20496

Query Match 4.1%; Score 8; DB 4; Length 444;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 IALGLLLA 18
Db 162 IALGLLLA 169

RESULT 12
US-09-252-991A-23790
; Sequence 23790, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23790
; LENGTH: 563
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23790

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Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GLLLATPA 21
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Db 60 GLLLATPA 67

RESULT 13
US-09-320-878-12
; Sequence 12, Application US/09320878A
; Patent No. 6117659
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary C.
; APPLICANT: MCDANIEL, Robert
; APPLICANT: TANG, Li
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 300622002120
; CURRENT APPLICATION NUMBER: US/09/320,878A
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: CIP OF 09/141,908
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247
; EARLIER FILING DATE: 1997-04-30
; EARLIER APPLICATION NUMBER: 60/119,139
; EARLIER FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: 60/100,880
; EARLIER FILING DATE: 1998-09-22
; EARLIER APPLICATION NUMBER: 60/087,080
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
US-09-320-878-12

Query Match 4.1%; Score 8; DB 3; Length 769;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GLLLATPA 21
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Db 285 GLLLATPA 292

RESULT 14
US-09-141-908-10
; Sequence 10, Application US/09141908
; Patent No. 6503741
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary
; APPLICANT: MCDANIEL, Robert
; APPLICANT: TANG, Li

; TITLE OF INVENTION: Combinatorial Polyketide Libraries Produced Using a
; TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold
; FILE REFERENCE: 300622002100
; CURRENT APPLICATION NUMBER: US/09/141,908
; CURRENT FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247
; EARLIER FILING DATE: 1997-04-30
; EARLIER APPLICATION NUMBER: PROV. 60/076,919
; EARLIER FILING DATE: 1998-03-05
; EARLIER APPLICATION NUMBER: PROV. 60/087,080
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
US-09-141-908-10

Query Match 4.1%; Score 8; DB 4; Length 769;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GLLLATPA 21
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Db 285 GLLLATPA 292

RESULT 15
US-09-657-440-12
; Sequence 12, Application US/09657440
; Patent No. 6509455
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary C.
; APPLICANT: MCDANIEL, Robert
; APPLICANT: TANG, Li
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 300622002120
; CURRENT APPLICATION NUMBER: US/09/657,440
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 09/320,878
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: CIP OF 09/141,908
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
US-09-657-440-12

Query Match 4.1%; Score 8; DB 4; Length 769;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GLLLATPA 21
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Db 285 GLLLATPA 292

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Job time : 37.8844 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2005, 19:08:40 ; Search time 107.222 Seconds
(without alignments)
700.186 Million cell updates/sec

Title: US-10-030-937-9
Perfect score: 193
Sequence: 1 MQSILMQAPLLIALGILLATP.....LSSGKRLGCIKIAASLKGI 193

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1741741 seqs, 388992284 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	112	58.0	193	15 US-10-170-385-389	Sequence 389, App
2	112	58.0	193	16 US-10-723-860-529	Sequence 529, App
3	61	31.6	61	9 US-09-864-761-34809	Sequence 34809, A
4	11	5.7	11	9 US-09-791-378-579	Sequence 579, App
5	11	5.7	11	11 US-09-791-377-579	Sequence 579, App
6	9	4.7	262	9 US-09-765-272-98	Sequence 98, Appl
7	9	4.7	270	9 US-09-765-272-206	Sequence 206, App
8	9	4.7	291	17 US-10-472-928-4348	Sequence 4348, Ap
9	9	4.7	328	18 US-10-617-320-3318	Sequence 3318, Ap
10	8	4.1	8	9 US-09-791-378-578	Sequence 578, App
11	8	4.1	8	11 US-09-791-377-578	Sequence 578, App

12	8	4.1	100	15 US-10-424-599-228216	Sequence 228216,
13	8	4.1	110	16 US-10-425-115-305353	Sequence 305353,
14	8	4.1	170	10 US-09-804-014A-37	Sequence 37, Appl
15	8	4.1	323	16 US-10-739-930-5722	Sequence 5722, Ap
16	8	4.1	466	16 US-10-437-963-119990	Sequence 119990,
17	8	4.1	574	16 US-10-324-967-36	Sequence 36, Appl
18	8	4.1	589	15 US-10-424-599-245422	Sequence 245422,
19	8	4.1	769	10 US-09-793-708-12	Sequence 12, Appl
20	8	4.1	769	14 US-10-201-365-10	Sequence 10, Appl
21	8	4.1	769	14 US-10-160-539-12	Sequence 12, Appl
22	8	4.1	769	17 US-10-468-828-12	Sequence 12, Appl
23	8	4.1	809	9 US-09-861-289-24	Sequence 24, Appl
24	8	4.1	809	9 US-09-860-846-24	Sequence 24, Appl
25	8	4.1	809	10 US-09-988-384B-24	Sequence 24, Appl
26	8	4.1	809	10 US-09-836-821-24	Sequence 24, Appl
27	8	4.1	809	14 US-10-271-889-24	Sequence 24, Appl
28	8	4.1	809	16 US-10-398-605-24	Sequence 24, Appl
29	8	4.1	1308	16 US-10-437-963-186215	Sequence 186215,
30	8	4.1	3782	9 US-09-861-289-4	Sequence 4, Appl
31	8	4.1	3782	9 US-09-860-846-4	Sequence 4, Appl
32	8	4.1	3782	10 US-09-988-384B-4	Sequence 4, Appl
33	8	4.1	3782	10 US-09-836-821-4	Sequence 4, Appl
34	8	4.1	3782	14 US-10-271-889-47	Sequence 47, Appl
35	8	4.1	3782	16 US-10-398-605-4	Sequence 4, Appl
36	7	3.6	23	17 US-10-828-559-3	Sequence 3, Appl
37	7	3.6	39	11 US-09-833-245-1222	Sequence 1222, Ap
38	7	3.6	39	11 US-09-833-245-1224	Sequence 1224, Ap
39	7	3.6	53	15 US-10-424-599-268608	Sequence 268608,
40	7	3.6	54	16 US-10-425-115-220040	Sequence 220040,
41	7	3.6	60	15 US-10-424-599-208921	Sequence 208921,
42	7	3.6	60	15 US-10-424-599-241819	Sequence 241819,
43	7	3.6	73	14 US-10-106-698-6961	Sequence 6961, Ap
44	7	3.6	83	15 US-10-425-114-61932	Sequence 61932, A
45	7	3.6	84	16 US-10-425-115-202828	Sequence 202828,

ALIGNMENTS

RESULT 1
US-10-170-385-389
; Sequence 389, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-389

Query Match 58.0%; Score 112; DB 15; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.9e-99;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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; SEQ ID NO 579
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-579

Query Match
Best Local Similarity 5.7%; Score 11; DB 9; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 TYGLPCHCPFK 141
Db 1 TYGLPCHCPFK 11

RESULT 5
US-09-791-377-579
; Sequence 579, Application US/09791377
; Publication No. US20040110938A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 9195-060-999
; CURRENT APPLICATION NUMBER: US/09/791,377
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 579
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-377-579

Query Match
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 TYGLPCHCPFK 141
Db 1 TYGLPCHCPFK 11

RESULT 6
US-09-765-272-98
; Sequence 98, Application US/09765272
; Patent No. US20020061545A1
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
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```
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 262 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 98:
US-09-765-272-98

Query Match
Best Local Similarity 4.7%; Score 9; DB 9; Length 262;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 LSVVGSTSV 74
Db 155 LSVVGSTSV 163

RESULT 7
US-09-765-272-206
; Sequence 206, Application US/09765272
; Patent No. US20020061545A1
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-09-765-272-206

Query Match
Best Local Similarity 4.7%; Score 9; DB 9; Length 270;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 66 LSVVGSTSV 74
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Db 163 LSVVGSTSV 171

RESULT 8
US-10-472-928-4348
; Sequence 4348, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026926W0
; CURRENT APPLICATION NUMBER: US/10/472,928
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107658.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4348
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; OTHER INFORMATION: phosphate ABC transporter, phosphate-binding protein (psts)
; OTHER INFORMATION: Cellular location: lipoprotein
; OTHER INFORMATION: Similar to strain R6 sequence 15903936 (e-160)
US-10-472-928-4348

Query Match 4.7%; Score 9; DB 17; Length 291;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 LSVVGSTSV 74
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Db 184 LSVVGSTSV 192

RESULT 9
US-10-617-320-3318
; Sequence 3318, Application US/10617320
; Publication No. US20050136404A1
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/617,320
; FILING DATE: 10-Jul-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke

; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3318:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...328
; SEQUENCE DESCRIPTION: SEQ ID NO: 3318:
US-10-617-320-3318

Query Match 4.7%; Score 9; DB 18; Length 328;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 LSVVGSTSV 74
| | | | | | | | | |
Db 221 LSVVGSTSV 229

RESULT 10
US-09-791-378-578
; Sequence 578, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF SCHIZOPHRENIA
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 578
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-578

Query Match 4.1%; Score 8; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 EVAGLWIK 96
| | | | | | | | | |
Db 1 EVAGLWIK 8

RESULT 11
US-09-791-377-578
; Sequence 578, Application US/09791377
; Publication No. US20040110938A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF SCHIZOPHRENIA
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-060-999
; CURRENT APPLICATION NUMBER: US/09/791,377
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 578

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-791-377-578

Query Match

4.1%; Score 8; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 EVAGLWIK 96

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Db 1 EVAGLWIK 8

RESULT 12

US-10-424-599-228216

; Sequence 228216, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 228216

; LENGTH: 100

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_48107C.1.pep

US-10-424-599-228216

Query Match

4.1%; Score 8; DB 15; Length 100;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 STSVPLSS 78

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Db 10 STSVPLSS 17

RESULT 13

US-10-425-115-305353

; Sequence 305353, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 305353

; LENGTH: 110

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_41551C.1.pep

US-10-425-115-305353

Query Match

4.1%; Score 8; DB 16; Length 110;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 IRSLTLEP 55

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Db 19 IRSLTLEP 26

RESULT 14

US-09-804-014A-37

; Sequence 37, Application US/09804014A

; Publication No. US20030064489A1

; GENERAL INFORMATION:

; APPLICANT: Li, Li

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Vernet, Corine

; APPLICANT: Fernandes, Elma

; APPLICANT: Shimkets, Richard

; APPLICANT: Spaderna, Steven

; APPLICANT: Majumder, Kumud

; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same

; FILE REFERENCE: 15966-721 US

; CURRENT APPLICATION NUMBER: US/09/804,014A

; CURRENT FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: 60/188,316

; PRIOR FILING DATE: 2000-03-10

; PRIOR APPLICATION NUMBER: 60/188,277

; PRIOR FILING DATE: 2000-03-10

; PRIOR APPLICATION NUMBER: 60/189,139

; PRIOR FILING DATE: 2000-03-14

; PRIOR APPLICATION NUMBER: 60/189,140

; PRIOR FILING DATE: 2000-03-14

; PRIOR APPLICATION NUMBER: 60/190,401

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: 60/190,231

; NUMBER OF SEQ ID NOS: 75

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 37

; LENGTH: 170

; TYPE: PRT

; ORGANISM: Bos taurus

US-09-804-014A-37

Query Match

4.1%; Score 8; DB 10; Length 170;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 LEKEVAGL 93

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Db 107 LEKEVAGL 114

RESULT 15

US-10-739-930-5722

; Sequence 5722, Application US/10739930

; Publication No. US20040216190A1

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH

; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

; FILE REFERENCE: 38-21(53377)B

; CURRENT APPLICATION NUMBER: US/10/739,930

; CURRENT FILING DATE: 2003-12-18

; NUMBER OF SEQ ID NOS: 11088

; SEQ ID NO 5722

; LENGTH: 323

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; OTHER INFORMATION: Clone ID: ARATH-23APR03-C126388_1.p

US-10-739-930-5722

Query Match

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Best Local Similarity 100.0%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 LEKEVAGL 93
| | | | |
Db 149 LEKEVAGL 156

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Job time : 108.222 secs

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OM protein - nucleic search, using frame_plus_p2n model

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(without alignments)
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Perfect score: 94
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Delop 6.0 , Delext 7.0

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20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	85	90.4	546	13	US-10-027-632-207798 Sequence 207798,
2	85	90.4	546	13	US-10-027-632-207799 Sequence 207799,
3	85	90.4	546	13	US-10-027-632-207800 Sequence 207800,
4	85	90.4	546	13	US-10-027-632-207801 Sequence 207801,
5	85	90.4	546	17	US-10-027-632-207798 Sequence 207798,
6	85	90.4	546	17	US-10-027-632-207799 Sequence 207799,
7	85	90.4	546	17	US-10-027-632-207800 Sequence 207800,
8	85	90.4	546	17	US-10-027-632-207801 Sequence 207801,
9	85	90.4	953	20	US-10-723-860-528 Sequence 528, App
10	85	90.4	1935	10	US-09-971-392-102 Sequence 102, App
11	85	90.4	2384	9	US-09-822-849A-53 Sequence 53, Appl
12	85	90.4	2436	9	US-09-954-531-380 Sequence 380, App
13	85	90.4	2436	10	US-09-525-978B-81 Sequence 81, Appl
14	85	90.4	2436	21	US-10-843-641A-1447 Sequence 1447, Ap
15	85	90.4	2478	17	US-10-170-385-390 Sequence 390, App
16	85	90.4	3988	20	US-10-723-860-5187 Sequence 5187, Ap
17	82	87.2	1983	17	US-10-388-934-167 Sequence 167, App
C 18	58	61.7	857	13	US-10-027-632-164063 Sequence 164063,
C 19	58	61.7	857	13	US-10-027-632-164064 Sequence 164064,
C 20	58	61.7	857	13	US-10-027-632-164065 Sequence 164065,
C 21	58	61.7	857	17	US-10-027-632-164063 Sequence 164063,
C 22	58	61.7	857	17	US-10-027-632-164064 Sequence 164064,
C 23	58	61.7	857	17	US-10-027-632-164065 Sequence 164065,
24	57	60.6	380	10	US-09-764-891-2290 Sequence 2290, Ap
25	57	60.6	577	17	US-10-264-049-436 Sequence 436, App
26	55	58.5	580	13	US-10-027-632-91348 Sequence 91348, A
27	55	58.5	580	13	US-10-027-632-317712 Sequence 317712,
28	55	58.5	580	17	US-10-027-632-91348 Sequence 91348, A
29	55	58.5	580	17	US-10-027-632-317712 Sequence 317712,
30	50.5	53.7	400660	19	US-10-388-838-68 Sequence 68, Appl
31	50	53.2	2243	17	US-10-108-260A-301 Sequence 301, App
C 32	50	53.2	2367	18	US-10-267-502-81 Sequence 81, Appl
C 33	50	53.2	2452	17	US-10-094-749-87 Sequence 87, Appl
34	50	53.2	383432	22	US-10-737-082-34 Sequence 34, Appl
35	50	53.2	383432	22	US-10-765-790-34 Sequence 34, Appl
C 36	49.5	52.7	600	22	US-10-972-079-45839 Sequence 45839, A
37	49	52.1	653	13	US-10-027-632-121823 Sequence 121823,
38	49	52.1	653	17	US-10-027-632-121823 Sequence 121823,
C 39	49	52.1	1197	18	US-10-424-599-20544 Sequence 20544, A
C 40	49	52.1	1493	18	US-10-424-599-78156 Sequence 78156, A
C 41	49	52.1	1701	18	US-10-335-977-3769 Sequence 3769, Ap
C 42	49	52.1	1704	18	US-10-335-977-3768 Sequence 3768, Ap
C 43	49	52.1	6306	18	US-10-433-794-38 Sequence 38, Appl
C 44	49	52.1	6629	17	US-10-353-690-35 Sequence 35, Appl
C 45	49	52.1	6629	17	US-10-172-118-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-027-632-207798
; Sequence 207798, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 10827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483

```

; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 207798
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-207798

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Alignment Scores:		
Pred. No.:	1.82e-05	546
Score:	85.00	15
Percent Similarity:	93.75%	0
Best Local Similarity:	93.75%	1
Query Match:	90.43%	0
DB:	13	0
	Length:	546
	Matches:	15
	Conservative:	0
	Mismatches:	1
	Indels:	0
	Gaps:	0

US-10-030-937-68 (1-16) x US-10-027-632-207798 (1-546)

Qy 1 PheSerTirAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
 |||||
Pb 276 TTTTCCTGGATAACTGTGATGAAGGGAAGSACCCCTCGCGTGATCAGA 323

RESULT 2

US-10-027-632-207799
; Sequence 207799, Application US/10027632
; Publication No. US2002019837A1
: GENERAL INFORMATION:

Alignment Scores:		
Pred. No.:	1.82e-05	546
Score:	85.00	15
Percent Similarity:	93.75%	0
Best Local Similarity:	93.75%	1
Query Match:	90.43%	0
DB:	13	0
	Length:	
	Matches:	
	Conservative:	
	Mismatches:	
	Indels:	
	Gaps:	

US-10-030-937-68 (1-16) x US-10-027-632-207799 (1-546)

1 PheSerTrpAspAsnCysPheGluGlyLysAspProLalaValIleArg 16
276 TTTTCTGGGATAACTGTGATGAAGGAAGGACCCCTGGGTGATCAGA 323

RESULT 3

US-10-027-632-207800
; Sequence 207800, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:

US-10-030-937-68 (1-16) x US-10-027-632-207800 (1-546)

1 PheSerTirpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
276 TTTTCCTGGATAACTGTGATGAAGGGAAGGACCCCTCGGTGATCAGA 323

RESULT 4

US-10-027-632-207801
; Sequence 207801, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:

; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ;

US-10-030-937-68 (1-16) x US-10-027-632-207799 (1-546)

; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207801
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-207801

Alignment Scores:
Pred. No.: 1.82e-05 Length: 546
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: 13 Gaps: 0

US-10-030-937-68 (1-16) x US-10-027-632-207801 (1-546)

Qy 1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
|||||
Db 276 TTTCTCTGGGATAACTGTGATGAAGGAAGGACCCCTGCGGTGATCAGA 323

RESULT 5

US-10-027-632-207798
; Sequence 207798, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207798
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-207798

Alignment Scores:
Pred. No.: 1.82e-05 Length: 546
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: 17 Gaps: 0

US-10-030-937-68 (1-16) x US-10-027-632-207798 (1-546)

Qy 1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
|||||
Db 276 TTTCTCTGGGATAACTGTGATGAAGGAAGGACCCCTGCGGTGATCAGA 323

RESULT 6

US-10-027-632-207799
; Sequence 207799, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207799
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-207799

Alignment Scores:

Pred. No.: 1.82e-05 Length: 546
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: 17 Gaps: 0

US-10-030-937-68 (1-16) x US-10-027-632-207799 (1-546)

Qy 1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
|||||
Db 276 TTTCTCTGGGATAACTGTGATGAAGGAAGGACCCCTGCGGTGATCAGA 323

RESULT 7

US-10-027-632-207800
; Sequence 207800, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207798
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-207798

Alignment Scores:

Pred. No.: 1.82e-05 Length: 546
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: 17 Gaps: 0

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 207800
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-207800

Alignment Scores:
Pred. No.:      1.82e-05      Length:      546
Score:          85.00        Matches:      15
Percent Similarity: 93.75%    Conservative: 0
Best Local Similarity: 93.75% Mismatches:      1
Query Match:    90.43%       Indels:        0
DB:             17          Gaps:          0

US-10-030-937-68 (1-16) x US-10-027-632-207800 (1-546)

Qy      1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
      |||||||
Db      276 TTTTCCTGGGATAACTGTGATGAAGGGAAGGACCCCTGCGGTGATCAGA 323

RESULT 8
US-10-027-632-207801
; Sequence 207801, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 10827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 207801
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-207801

Alignment Scores:
Pred. No.:      1.82e-05      Length:      546
Score:          85.00        Matches:      15
Percent Similarity: 93.75%    Conservative: 0
Best Local Similarity: 93.75% Mismatches:      1
Query Match:    90.43%       Indels:        0
DB:             17          Gaps:          0

US-10-030-937-68 (1-16) x US-10-027-632-207801 (1-546)

Qy      1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
      |||||||
Db      276 TTTTCCTGGGATAACTGTGATGAAGGGAAGGACCCCTGCGGTGATCAGA 323

RESULT 9
US-10-723-860-528
; Sequence 528, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
```

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; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 528
; LENGTH: 953
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-528

Alignment Scores:
Pred. No.:      3.39e-05      Length:      953
Score:          85.00        Matches:      15
Percent Similarity: 93.75%    Conservative: 0
Best Local Similarity: 93.75% Mismatches:      1
Query Match:    90.43%       Indels:        0
DB:             20          Gaps:          0

US-10-030-937-68 (1-16) x US-10-723-860-528 (1-953)

Qy      1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
      |||||||
Db      190 TTTTCCTGGGATAACTGTGATGAAGGGAAGGACCCCTGCGGTGATCAGA 237

RESULT 10
US-09-971-392-102
; Sequence 102, Application US/09971392
; Publication No. US20030134283A1
; GENERAL INFORMATION:
; APPLICANT: Peterson, David P.
; APPLICANT: Pearson, Cecelia I.
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION
; FILE REFERENCE: PA-0029 US
; CURRENT APPLICATION NUMBER: US/09/971,392
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/237,652
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PERL Program
; SEQ ID NO 102
; LENGTH: 1935
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Template ID: 977615.8
US-09-971-392-102

Alignment Scores:
Pred. No.:      7.46e-05      Length:      1935
Score:          85.00        Matches:      15
Percent Similarity: 93.75%    Conservative: 0
Best Local Similarity: 93.75% Mismatches:      1
Query Match:    90.43%       Indels:        0
DB:             10          Gaps:          0

US-10-030-937-68 (1-16) x US-09-971-392-102 (1-1935)

Qy      1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
      |||||||
Db      201 TTTTCCTGGGATAACTGTGATGAAGGGAAGGACCCCTGCGGTGATCAGA 248

RESULT 11
US-09-822-849A-53
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; Sequence 53, Application US/09822849A
; Patent No. US20020045170A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6403
; CURRENT APPLICATION NUMBER: US/09/822,849A
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/195,582
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 598
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 2384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-849A-53

Alignment Scores:
Pred. No.:          9.41e-05          Length:          2384
Score:              85.00             Matches:          15
Percent Similarity: 93.75%            Conservative:    0
Best Local Similarity: 93.75%          Mismatches:      1
Query Match:        90.43%            Indels:          0
DB:                 9                Gaps:            0

US-10-030-937-68 (1-16) x US-09-822-849A-53 (1-2384)

QY      1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
      |||||||
Db      112 TTTTCCTGGGATAACTGTGATGAAGGAAGGACCCCTGCGGTGATCAGA 159

RESULT 12
US-09-954-531-380
; Sequence 380, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 380
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-380

Alignment Scores:
Pred. No.:          9.64e-05          Length:          2436
Score:              85.00             Matches:          15
Percent Similarity: 93.75%            Conservative:    0
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```
Best Local Similarity: 93.75%          Mismatches:      1
Query Match:        90.43%            Indels:          0
DB:                 9                Gaps:            0

US-10-030-937-68 (1-16) x US-09-954-531-380 (1-2436)

QY      1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
      |||||||
Db      158 TTTTCCTGGGATAACTGTGATGAAGGAAGGACCCCTGCGGTGATCAGA 205

RESULT 13
US-09-525-978B-81
; Sequence 81, Application US/09525978B
; Publication No. US20030049722A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Caras, Ingrid W.
; APPLICANT: Hevezi, Peter
; APPLICANT: Wilson, Keith
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING MACROPHAGE DEVELOPMENT
; TITLE OF INVENTION: RELATED DISORDERS, COMPOSITIONS, AND METHODS OF
; TITLE OF INVENTION: SCREENING FOR MACROPHAGE DEVELOPMENT MODULATORS
; FILE REFERENCE: A-67413-1/DJB/JJD
; CURRENT APPLICATION NUMBER: US/09/525,978B
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: USSN 60/124,530
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-525-978B-81

Alignment Scores:
Pred. No.:          9.64e-05          Length:          2436
Score:              85.00             Matches:          15
Percent Similarity: 93.75%            Conservative:    0
Best Local Similarity: 93.75%          Mismatches:      1
Query Match:        90.43%            Indels:          0
DB:                 10               Gaps:            0

US-10-030-937-68 (1-16) x US-09-525-978B-81 (1-2436)

QY      1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
      |||||||
Db      158 TTTTCCTGGGATAACTGTGATGAAGGAAGGACCCCTGCGGTGATCAGA 205

RESULT 14
US-10-843-641A-1447
; Sequence 1447, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
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; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1447
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-1447

Alignment Scores:
Pred. No.: 9.64e-05 Length: 2436
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: 21 Gaps: 0

US-10-030-937-68 (1-16) x US-10-843-641A-1447 (1-2436)

Qy 1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
|||||
Db 158 TTTTCCTGGGATAACTGTGATGAAGGAAGGACCCTGCGGTGATCAGA 205

RESULT 15

US-10-170-385-390
; Sequence 390, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 53268200100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390
; LENGTH: 2478
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-170-385-390

Alignment Scores:
Pred. No.: 9.82e-05 Length: 2478
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: 17 Gaps: 0

US-10-030-937-68 (1-16) x US-10-170-385-390 (1-2478)

Qy 1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
|||||

Db 195 TTTTCCTGGGATAACTGTGATGAAGGAAGGACCCTGCGGTGATCAGA 242

Search completed: July 27, 2005, 22:48:02
Job time : 100.631 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 27, 2005, 19:27:35 ; Search time 312.231 Seconds
(without alignments)
1011.435 Million cell updates/sec

Title: US-10-030-937-9
Perfect score: 193
Sequence: 1 MQLMQAPLLIALGLLATP.....LSSGKRLGCIKIAASLKGI 193

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Word size: 1
Total number of hits satisfying chosen parameters: 2400006

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10030937 @CGN_1_1_116 @runat_26072005_132301_10709 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	5.2	1089	US-09-902-540-4802	Sequence 4802, Ap
2	10	5.2	29103	US-09-902-540-1236	Sequence 1236, Ap
3	9	4.7	787	US-08-961-083-97	Sequence 97, Appl
4	9	4.7	787	US-09-536-784-97	Sequence 97, Appl
5	9	4.7	811	US-08-961-083-205	Sequence 205, App
6	9	4.7	811	US-09-536-784-205	Sequence 205, App
7	9	4.7	876	US-09-583-110-1540	Sequence 1540, Ap
8	9	4.7	987	US-09-107-433-715	Sequence 715, App
9	9	4.7	12127	US-08-961-527-148	Sequence 148, App
10	9	4.7	48794	US-09-949-016-15637	Sequence 15637, A
c 11	8	4.1	462	US-09-252-991A-546	Sequence 546, App
12	8	4.1	601	US-09-949-016-39132	Sequence 39132, A

13	8	4.1	601	4	US-09-949-016-53584	Sequence 53584, A
14	8	4.1	601	4	US-09-949-016-61592	Sequence 61592, A
15	8	4.1	601	4	US-09-949-016-61593	Sequence 61593, A
16	8	4.1	601	4	US-09-949-016-61714	Sequence 61714, A
17	8	4.1	601	4	US-09-949-016-61715	Sequence 61715, A
18	8	4.1	601	4	US-09-949-016-84688	Sequence 84688, A
19	8	4.1	601	4	US-09-949-016-91993	Sequence 91993, A
20	8	4.1	601	4	US-09-949-016-91994	Sequence 91994, A
c 21	8	4.1	601	4	US-09-949-016-158399	Sequence 158399,
c 22	8	4.1	601	4	US-09-949-016-158400	Sequence 158400,
23	8	4.1	711	4	US-09-774-639-24	Sequence 24, Appl
c 24	8	4.1	858	4	US-09-252-991A-3981	Sequence 3981, Ap
25	8	4.1	1314	4	US-09-252-991A-7168	Sequence 7168, Ap
26	8	4.1	1335	4	US-09-252-991A-3925	Sequence 3925, Ap
c 27	8	4.1	1395	4	US-09-711-164-270	Sequence 270, App
c 28	8	4.1	1395	4	US-09-492-709A-121	Sequence 121, App
c 29	8	4.1	1456	3	US-09-308-406-1	Sequence 1, Appl
30	8	4.1	1458	4	US-09-252-991A-570	Sequence 570, App
c 31	8	4.1	1482	4	US-09-252-991A-4050	Sequence 4050, Ap
32	8	4.1	1605	4	US-09-252-991A-3897	Sequence 3897, Ap
c 33	8	4.1	1677	4	US-09-252-991A-7476	Sequence 7476, Ap
34	8	4.1	1692	4	US-09-252-991A-7219	Sequence 7219, Ap
c 35	8	4.1	2223	4	US-09-252-991A-4015	Sequence 4015, Ap
36	8	4.1	2401	3	US-09-320-878-20	Sequence 20, Appl
37	8	4.1	2401	4	US-09-141-908-9	Sequence 9, Appl
38	8	4.1	2401	4	US-09-657-440-20	Sequence 20, Appl
39	8	4.1	2430	3	US-09-105-537-23	Sequence 23, Appl
c 40	8	4.1	2772	3	US-08-936-135-1	Sequence 1, Appl
c 41	8	4.1	2772	4	US-09-439-711C-1	Sequence 1, Appl
42	8	4.1	2881	2	US-08-570-227A-1	Sequence 1, Appl
43	8	4.1	2881	3	US-09-077-991-1	Sequence 1, Appl
44	8	4.1	3125	4	US-09-949-016-1081	Sequence 1081, Ap
45	8	4.1	3241	3	US-09-434-288-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-902-540-4802
; Sequence 4802, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4802
; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4802

Alignment Scores:
Pred. No.: 0.86 Length: 1089
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-9 (1-193) x US-09-902-540-4802 (1-1089)

Qy 8 ProLeuLeuIleAlaLeuGlyLeuLeu 17

Db 691 CCGCTGCTCATCGCCCTGGCCTGCTGCTG 720

US-10-030-937-9 (1-193) x US-09-536-784-97 (1-787)

QY 66 LeuSerValValGlySerThrSerVal 74
|||||
Db 464 TTGTCGTGTAGGTTCCACTTCAGTA 490

RESULT 5

US-08-961-083-205
; Sequence 205, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/961,083
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 205:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 811 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-961-083-205

Alignment Scores:
Pred. No.: 6.98 Length: 811
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.66% Indels: 0
DB: 3 Gaps: 0

US-10-030-937-9 (1-193) x US-08-961-083-205 (1-811)

QY 66 LeuSerValValGlySerThrSerVal 74
|||||
Db 488 TTGTCGTGTAGGTTCCACTTCAGTA 514

RESULT 6

US-09-536-784-205
; Sequence 205, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 205:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 811 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-09-536-784-205

Alignment Scores:
Pred. No.: 6.98 Length: 811
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.66% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-9 (1-193) x US-09-536-784-205 (1-811)

QY 66 LeuSerValValGlySerThrSerVal 74
|||||
Db 488 TTGTCGTGTAGGTTCCACTTCAGTA 514

RESULT 7

US-09-583-110-1540
; Sequence 1540, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 1540
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-1540
Alignment Scores:
Pred. No.: 7.53 Length: 876

Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.66% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-9 (1-193) x US-09-583-110-1540 (1-876)

Qy 66 LeuSerValValGlySerThrSerVal 74
Db 550 TTGTCGTGTAGGTTCCACTTCAGTA 576

RESULT 8

US-09-107-433-715
; Sequence 715, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 715:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 987 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...987
; SEQUENCE DESCRIPTION: SEQ ID NO: 715:
US-09-107-433-715
Alignment Scores:
Pred. No.: 8.46 Length: 987
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.66% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-9 (1-193) x US-09-107-433-715 (1-987)
Qy 66 LeuSerValValGlySerThrSerVal 74
Db 661 TTGTCGTGTAGGTTCCACTTCAGTA 687

RESULT 9

US-08-961-527-148
; Sequence 148, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12127 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-961-527-148
Alignment Scores:
Pred. No.: 97.8 Length: 12127
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.66% Indels: 0
DB: 3 Gaps: 0
US-10-030-937-9 (1-193) x US-08-961-527-148 (1-12127)
Qy 66 LeuSerValValGlySerThrSerVal 74
Db 624 TTGTCGTGTAGGTTCCACTTCAGTA 650
RESULT 10
US-09-949-016-15637
; Sequence 15637, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15637
; LENGTH: 48794
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(48794)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15637

Alignment Scores:
Pred. No.: 380 Length: 48794
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.66% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-9 (1-193) x US-09-949-016-15637 (1-48794)

QY 71 SerThrSerValProLeuSerSerPro 79
|||||
Db 37782 TCCACCTCAGTTCCTTTATCTTCCT 37808

RESULT 11

US-09-252-991A-546/c
; Sequence 546, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 546
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-546

Alignment Scores:
Pred. No.: 43.7 Length: 462
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.15% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-9 (1-193) x US-09-252-991A-546 (1-462)

QY 71 SerThrSerValProLeuSerSer 78
|||||
Db 395 TCTACGTCAGTTCCTCGTTTCGTCA 372

RESULT 12

US-09-949-016-39132
; Sequence 39132, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39132
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-39132

Alignment Scores:
Pred. No.: 56.5 Length: 601
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.15% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-9 (1-193) x US-09-949-016-39132 (1-601)

QY 86 LeuGluLysGluValAlaGlyLeu 93
|||||
Db 188 CTGGAAGAGGAGTGGCCGGGTG 211

RESULT 13

US-09-949-016-53584
; Sequence 53584, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53584
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-53584

Alignment Scores:
Pred. No.: 56.5 Length: 601
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.15% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-9 (1-193) x US-09-949-016-53584 (1-601)

QY 175 SerSerSerGlyLysArgLeuGly 182
|||||
Db 173 TCAAGCAGTGGAAAGAGGCTGGC 196

RESULT 14

US-09-949-016-61592

; Sequence 61592, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 61592

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-61592

Alignment Scores:

Pred. No.: 56.5

Length: 601

Score: 8.00

Matches: 8

Percent Similarity: 100.00%

Conservative: 0

Best Local Similarity: 100.00%

Mismatches: 0

Query Match: 4.15%

Indels: 0

DB: 4

US-10-030-937-9 (1-193) x US-09-949-016-61592 (1-601)

Qy 67 SerValValGlySerThrSerVal 74

|||||

Db 475 TCCGTCGTTGGGTCCACCAGTGTG 498

RESULT 15

US-09-949-016-61593

; Sequence 61593, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 61593

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-61593

Alignment Scores:

Pred. No.: 56.5

Length: 601

Score: 8.00

Matches: 8

Percent Similarity: 100.00%

Conservative: 0

Best Local Similarity: 100.00%

Mismatches: 0

Query Match: 4.15%

Indels: 0

DB: 4

US-10-030-937-9 (1-193) x US-09-949-016-61593 (1-601)

Qy 67 SerValValGlySerThrSerVal 74

|||||

Db 227 TCCGTCGTTGGGTCCACCAGTGTG 250

Search completed: July 27, 2005, 22:54:19

Job time : 323.231 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
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Perfect score: 193
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4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
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13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
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17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:
22: /cgn2_6/ptodata/1/pubpna/US10J_NEW_PUB.seq:
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	112	58.0	953	20	US-10-723-860-528 Sequence 528, App
2	112	58.0	1935	10	US-09-971-392-102 Sequence 102, App
3	112	58.0	2384	9	US-09-822-849A-53 Sequence 53, Appl
4	112	58.0	2436	9	US-09-954-531-380 Sequence 380, App
5	112	58.0	2436	10	US-09-525-978B-81 Sequence 81, Appl
6	112	58.0	2436	21	US-10-843-641A-1447 Sequence 1447, Ap
7	112	58.0	2478	17	US-10-170-385-390 Sequence 390, App
8	112	58.0	3988	20	US-10-723-860-5187 Sequence 5187, Ap
C 9	61	31.6	475	9	US-09-864-761-1518 Sequence 1518, Ap
C 10	48	24.9	145	9	US-09-864-761-18277 Sequence 18277, A
11	40	20.7	448	11	US-09-969-034-4215 Sequence 4215, Ap
C 12	40	20.7	250000	16	US-10-225-810-26 Sequence 26, Appl
13	18	9.3	546	13	US-10-027-632-207798 Sequence 207798,
14	18	9.3	546	13	US-10-027-632-207799 Sequence 207799,
15	18	9.3	546	13	US-10-027-632-207800 Sequence 207800,
16	18	9.3	546	13	US-10-027-632-207801 Sequence 207801,
17	18	9.3	546	17	US-10-027-632-207798 Sequence 207798,
18	18	9.3	546	17	US-10-027-632-207799 Sequence 207799,
19	18	9.3	546	17	US-10-027-632-207800 Sequence 207800,
20	18	9.3	546	17	US-10-027-632-207801 Sequence 207801,
21	18	9.3	1983	17	US-10-388-934-167 Sequence 167, App
22	9	4.7	218	11	US-09-922-293-2287 Sequence 2287, Ap
C 23	9	4.7	455	13	US-10-027-632-202246 Sequence 202246,
C 24	9	4.7	455	17	US-10-027-632-202246 Sequence 202246,
25	9	4.7	649	18	US-10-425-114-7785 Sequence 7785, Ap
26	9	4.7	787	9	US-09-765-272-97 Sequence 97, Appl
27	9	4.7	811	9	US-09-765-272-205 Sequence 205, App
28	9	4.7	873	21	US-10-472-928-4347 Sequence 4347, Ap
29	9	4.7	987	22	US-10-617-320-715 Sequence 715, App
30	9	4.7	1051	18	US-10-424-599-38496 Sequence 38496, A
31	9	4.7	12127	8	US-08-961-527-148 Sequence 148, App
32	9	4.7	12127	17	US-10-158-844-148 Sequence 148, App
33	9	4.7	2162598	21	US-10-472-928-4979 Sequence 4979, Ap
34	8	4.1	25	21	US-10-719-900-237828 Sequence 237828,
35	8	4.1	60	10	US-09-908-975-22643 Sequence 22643, A
C 36	8	4.1	195	9	US-09-864-761-18267 Sequence 18267, A
C 37	8	4.1	223	18	US-10-424-599-102858 Sequence 102858,
C 38	8	4.1	274	20	US-10-425-115-5227 Sequence 5227, Ap
C 39	8	4.1	301	21	US-10-696-639-2552 Sequence 2552, Ap
C 40	8	4.1	319	9	US-09-864-761-20513 Sequence 20513, A
C 41	8	4.1	331	20	US-10-425-115-120690 Sequence 120690,
42	8	4.1	391	11	US-09-864-408A-4241 Sequence 4241, Ap
43	8	4.1	406	9	US-09-960-352-14056 Sequence 14056, A
44	8	4.1	420	18	US-10-424-599-85374 Sequence 85374, A
C 45	8	4.1	430	9	US-09-864-761-1508 Sequence 1508, Ap

ALIGNMENTS

RESULT 1

US-10-723-860-528
; Sequence 528, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 528
; LENGTH: 953
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-528

Alignment Scores:
Pred. No.: 1.63e-102 Length: 953
Score: 112.00 Matches: 152
Percent Similarity: 98.70% Conservative: 0
Best Local Similarity: 98.70% Mismatches: 1
Query Match: 58.03% Indels: 2
DB: 20 Gaps: 0

US-10-030-937-9 (1-193) x US-10-723-860-528 (1-953)

Qy 41 GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVal 60
Db 211 GAAGGGAAGGACCCCTGCGGTGATCAGAAGCCCTGACTCTGGAGCCTGACCCCATCGTCGTT 270
Qy 61 ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLeu 80
Db 271 CCTGGAATGTGACCCCTCAGTGTCTGGGAGGAGGAGTGTCCCTGAGTTCTCCTCTG 330
Qy 81 LysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCysThr 100
Db 331 AAGGTGGATTAGTTTTGGAGAGGAGGTGGCTGGCTCTGGATCAAGATCCCATGCACA 390
Qy 101 AspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIlePro 120
Db 391 GACTACATTTGGCAGCTGTACCTTTTGAACACTTCTGTGATGTGCTTGACATGTTAATCCT 450
Qy 121 ThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPhe 140
Db 451 ACTGGGAGCCCTGCCCAGAGCCCTGCGTACCTATGGGCTTCTTGCCACTGTCCCTTC 510
Qy 141 LysGluGlyThrTyrSerLeuProLysSerGluPheAla-ValProAspLeuGluLeuPr 160
Db 511 AAAGAAGGAACCTACTACTGCCCCAAGAGCGAATTTCGT-TGTGCCTGACCTGGAGCTGCC 569
Qy 160 oSerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysAr 180
Db 570 CAGTTGGCTCACCAACCGGAACCTACCGCATAGAGAGCGTCTTGAGCAGCAGTGGGAAGCG 629
Qy 180 gLeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle 193
Db 630 TCTGGGCTGCATCAAGATCGCTGCCTCTCTAAAGGGGCATA 669

RESULT 2
US-09-971-392-102
; Sequence 102, Application US/09971392
; Publication No. US20030134283A1
; GENERAL INFORMATION:
; APPLICANT: Peterson, David P.
; APPLICANT: Pearson, Cecelia I.
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION
; FILE REFERENCE: PA-0029 US
; CURRENT APPLICATION NUMBER: US/09/971,392
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/237,652
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PERL Program
; SEQ ID NO 102
; LENGTH: 1935
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Template ID: 977615.8
US-09-971-392-102
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Alignment Scores:
Pred. No.: 3.08e-102 Length: 1935
Score: 112.00 Matches: 152
Percent Similarity: 98.70% Conservative: 0
Best Local Similarity: 98.70% Mismatches: 1
Query Match: 58.03% Indels: 2
DB: 10 Gaps: 0

US-10-030-937-9 (1-193) x US-09-971-392-102 (1-1935)

Qy 41 GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVal 60
Db 222 GAAGGGAAGGACCCCTGCGGTGATCAGAAGCCCTGACTCTGGAGCCTGACCCCATCGTCGTT 281
Qy 61 ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLeu 80
Db 282 CCTGGAATGTGACCCCTCAGTGTCTGGGAGCAGCACCAAGTGTCCCTGAGTTCTCCTCTG 341
Qy 81 LysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCysThr 100
Db 342 AAGGTGGATTAGTTTTGGAGAGGAGGTGGCTGGCTCTGGATCAAGATCCCATGCACA 401
Qy 101 AspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIlePro 120
Db 402 GACTACATTTGGCAGCTGTACCTTTTGAACACTTCTGTGATGTGCTTGACATGTTAATCCT 461
Qy 121 ThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPhe 140
Db 462 ACTGGGAGCCCTGCCCAGAGCCCTGCGTACCTATGGGCTTCTTGCCACTGTGCTCCTTC 521
Qy 141 LysGluGlyThrTyrSerLeuProLysSerGluPheAla-ValProAspLeuGluLeuPr 160
Db 522 AAAGAAGGAACCTACTACTGCCCCAAGAGCGAATTTCGT-TGTGCCTGACCTGGAGCTGCC 580
Qy 160 oSerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysAr 180
Db 581 CAGTTGGCTCACCAACCGGAACCTACCGCATAGAGAGCGTCTTGAGCAGCAGTGGGAAGCG 640
Qy 180 gLeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle 193
Db 641 TCTGGGCTGCATCAAGATCGCTGCCTCTCTAAAGGGGCATA 680

RESULT 3
US-09-822-849A-53
; Sequence 53, Application US/09822849A
; Patent No. US20020045170A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fachtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6403
; CURRENT APPLICATION NUMBER: US/09/822,849A
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/195,582
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 598
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 2384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-849A-53

Alignment Scores:
Pred. No.: 3.72e-102 Length: 2384
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Score:	112.00	Matches:	152
Percent Similarity:	98.70%	Conservative:	0
Best Local Similarity:	98.70%	Mismatches:	1
Query Match:	58.03%	Indels:	2
DB:	9	Gaps:	0

US-10-030-937-9 (1-193) X US-09-822-849A-53 (1-2384)

Qy	41	GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleVal	60
Db	133	GAAGGGAAGGACCCCTGCGGTGATCAGAAGCCTGACTCTGGAGCCTGACCCCATCGTCGT	192
Qy	61	ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLeu	80
Db	193	CCTGGAATGTGACCCCTCAGTGTCTGGGCGAGCACAGTGTCCCTGAGTCTCTCTCTG	252
Qy	81	LysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCysThr	100
Db	253	AAGGTGGATTAGTTTGGAGAAGAGGTGGCTGGCTCTGGATCAAGATCCCATGCACA	312
Qy	101	AspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetIleuIlePro	120
Db	313	GACTACATGGCAGCTGTACCTTTGAACACTTCTGTGTATGTGCTTGACATGTAATTCCT	372
Qy	121	ThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPhe	140
Db	373	ACTGGGAGACCCCTGCCAGAGCCCTTCGTACCTATGGGCTTCCTTGCCACTGTCCCTTC	432
Qy	141	LysGluGlyThrTyrSerLeuProLysSerGluPheAla - ValProAspLeuGluLeuPr	160
Db	433	AAAGAAAGAAACCTACTCCTGCCCCAAGAGCGAATTCGT - TGTGCTGACCTGGAGCTGCC	491
Qy	160	oSerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysAr	180
Db	492	CAGTTGGCTCACCACCGGGAACCTACCGCATAGAGAGCGTCTCTGAGCAGCAGTGGGAAGCG	551
Qy	180	gLeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle	193
Db	552	TCTGGGCTGCATCAAGATCGCTGCCTCTCTAAAGGGGCATA	591

RESULT 4

US-09-954-531-380
; Sequence 380, Application US/09954531
; Patent No. US20020165180A1
: GENERAL INFORMATION:

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; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Candi
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 380
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-380

```

Alignment Scores:	
Pred. No.:	3.79e-102
Score:	112.00
Percent Similarity:	97.95%
Length:	2436
Matches:	191
Conservative:	0

Best Local Similarity:	97.95%	Mismatches:	2
Query Match:	58.03%	Indels:	4
DB:	9	Gaps:	0
US-10-030-937-9 (1-193) x US-09-954-531-380 (1-2436)			

Qy	1	MetGlnSerLeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrPro	20
Db	59	ATGCAGTCCCTGATGCAGGCTCCCTCCTGATCGCCCTGGGCTTGTCTTCGCGACCCCT	118
Qy	21	AlaGlnAlaHisLeuLysLysProSerGlnLeuSerSerPheSerTrpAspAsnCysPhe	40
Db	119	GGCAAGCCACCTGAAAAGCCATCCAGCTCAGTAGCTTTTCTGGGATAACTGTGA-	177
Qy	41	-GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVa	60
Db	178	TGAAGGGAAGGACCCCTCGGGTGATCAGAAGCCGTGACTCTGGAGCCTGACCCCATCGTCGT	237
Qy	60	lProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLe	80
Db	238	TCCTGGAAATGTGACCCCTCAGTGTCTGTGGGACGACCAGTGTCCCTTGAGTTCTCCTCT	297
Qy	80	uLysValAspLeuValLeuGluLysGluValAlaGlyLeuTirpileLysIleProCysTh	100
Db	298	GAAGTGGATTAGTTTGGAGAAGGAGGTGGCTGGCCTCTGGATCAAGATCCCATGCAC	357
Qy	100	rAspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIlePr	120
Db	358	AGACTACATGGCAGCTGTACCTTTGAACACTTCTGTGATGTGCTTGACATGTTAATTCC	417
Qy	120	oThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPh	140
Db	418	TACTGGGGAGCCCTGCCAGACCCCTCGGTACCTATGGGCTTCCTTGCCACTGTCCCTT	477
Qy	140	eLysGluGlyThrTyrSerLeuProLysSerGluPheAla - ValProAspLeuGluLeuP	160
Db	478	CAAAGAAGGAACCTACTACTGCCCAAGAGCGAATTTCGT - TGTGCCTGACCTGGAGTGCG	536
Qy	160	roSerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysA	180
Db	537	CCAGTTGGCTCACCAACCGGGAACATACCGCATAGAGAGCGTCTCTGAGCAGCAGTGGGAAGC	596
Qy	180	rgLeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle	193
Db	597	GTCTGGGCTGCATCAAGATCGCTGCCTCTCTAAAGGGGCATA	637

RESULT 5

US-09-525-978B-81
; Sequence 81, Application US/09525978B
; Publication No. US2003004972A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Caras, Ingrid W.
; APPLICANT: Hevezi, Peter
; APPLICANT: Wilson, Keith
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING MACROPHAGE DEVELOPMENT
; TITLE OF INVENTION: RELATED DISORDERS, COMPOSITIONS, AND METHODS OF
; TITLE OF INVENTION: SCREENING FOR MACROPHAGE DEVELOPMENT MODULATORS
; FILE REFERENCE: A-67413-1/DJB/JJD
; CURRENT APPLICATION NUMBER: US/09/525,978B
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: USSN 60/124,530
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-525-978B-81

Alignment Scores:
Pred. No.: 3.79e-102 Length: 2436

Score: 112.00 Matches: 191
Percent Similarity: 97.95% Conservative: 0
Best Local Similarity: 97.95% Mismatches: 2
Query Match: 58.03% Indels: 4
DB: 10 Gaps: 0

US-10-030-937-9 (1-193) x US-09-525-978B-81 (1-2436)

Qy 1 MetGlnSerLeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrPro 20
Db 59 ATGCAGTCCCTGATGAGGCTCCCTCCTGATCGCCCTGGGCTTGCTTCGCGACCCCT 118

Qy 21 AlaGlnAlaHisLeuLysProSerGlnLeuSerSerPheSerTrpAspAsnCysPhe 40
Db 119 GCGCAAGCCACCTGAAAAGCCATCCCAGCTCAGTAGCTTTTCTGGGATAACTGTGA- 177

Qy 41 -GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVa 60
Db 178 TGAAGGGAAGGACCCCTGCGGTGATCAGAAGCCTGACTCTGGAGCCTGACCCCATCGTGGT 237

Qy 60 lProGlyAanValThrLeuSerValValGlySerThrSerValProLeuSerSerProLe 80
Db 238 TCCTGGAATGTGACCCCTCAGTGTGCTGGGCAGCACCCAGTGTCCCCCTGAGTTCTCCTCT 297

Qy 80 uLysValAspLeuValLeuGluLysValAlaGlyLeuTrpIleLysIleProCysTh 100
Db 298 GAAGTGGATTAGTTTTGGAGAAGGAGTGGCTGGCCTCTGGATCAAGATCCCATGCAC 357

Qy 100 rAspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIlePr 120
Db 358 AGACTACATTGGCAGCTGTACCTTTGAACACTTCTGTGATGTCTTGACATGTTAATTC 417

Qy 120 oThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPh 140
Db 418 TACTGGGAGCCCTGCCAGAGCCCTGCGTACCTATGGGCTTCCTTGCCACTGTCCCTT 477

Qy 140 eLysGluGlyThrTyrSerLeuProLysSerGluPheAla-ValProAspLeuGluLeuP 160
Db 478 CAAAGAAGGAACCTACTACTGCCCAAGAGCGAATTCGT-TGTGCCTGACCTGGAGCTGC 536

Qy 160 roSerTrpLeuThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysA 180
Db 537 CCAGTTGGCTCACCCCGGGAACCTACCGCATAGAGAGCTCCTGAGCAGCAGTGGGAAGC 596

Qy 180 rgLeuGlyCysIleLysIleAlaAalaSerLeuLysGlyIle 193
Db 597 GTCTGGGCTGCATCAAGATCGCTGCCTCTCTAAAGGGGCATA 637

RESULT 6
US-10-843-641A-1447
; Sequence 1447, Application US/10843641A
; Publication No. US2005006454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28

; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1447
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-1447

Alignment Scores:
Pred. No.: 3.79e-102 Length: 2436
Score: 112.00 Matches: 191
Percent Similarity: 97.95% Conservative: 0
Best Local Similarity: 97.95% Mismatches: 2
Query Match: 58.03% Indels: 4
DB: 21 Gaps: 0

US-10-030-937-9 (1-193) x US-10-843-641A-1447 (1-2436)

Qy 1 MetGlnSerLeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrPro 20
Db 59 ATGCAGTCCCTGATGAGGCTCCCTCCTGATCGCCCTGGGCTTGCTTCGCGACCCCT 118

Qy 21 AlaGlnAlaHisLeuLysLysProSerGlnLeuSerSerPheSerTrpAspAsnCysPhe 40
Db 119 GCGCAAGCCACCTGAAAAGCCATCCCAGCTCAGTAGCTTTTCTGGGATAACTGTGA- 177

Qy 41 -GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVa 60
Db 178 TGAAGGGAAGGACCCCTGCGGTGATCAGAAGCCTGACTCTGGAGCCTGACCCCATCGTCT 237

Qy 60 lProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLe 80
Db 238 TCCTGGAATGTGACCCCTCAGTGTGCTGGGCAGCACCCAGTGTCCCCCTGAGTTCTCCTCT 297

Qy 80 uLysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCysTh 100
Db 298 GAAGTGGATTAGTTTTGGAGAAGGAGTGGCTGGCCTCTGGATCAAGATCCCATGCAC 357

Qy 100 rAspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIlePr 120
Db 358 AGACTACATTGGCAGCTGTACCTTTGAACACTTCTGTGATGTCTTGACATGTTAATTC 417

Qy 120 oThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPh 140
Db 418 TACTGGGAGCCCTGCCAGAGCCCTGCGTACCTATGGGCTTCCCTGACCATGTCCCTT 477

Qy 140 eLysGluGlyThrTyrSerLeuProLysSerGluPheAla-ValProAspLeuGluLeuP 160
Db 478 CAAAGAAGGAACCTACTACTGCCCAAGAGCGAATTCGT-TGTGCCTGACCTGGAGCTGC 536

Qy 160 roSerTrpLeuThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysA 180
Db 537 CCAGTTGGCTCACCCCGGGAACCTACCGCATAGAGAGCTCCTGAGCAGCAGTGGGAAGC 596

Qy 180 rgLeuGlyCysIleLysIleAlaAalaSerLeuLysGlyIle 193
Db 597 GTCTGGGCTGCATCAAGATCGCTGCCTCTCTAAAGGGGCATA 637

RESULT 7
US-10-170-385-390
; Sequence 390, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On

; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390
; LENGTH: 2478
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-170-385-390

Alignment Scores:
Pred. No.: 3.85e-102 Length: 2478
Score: 112.00 Matches: 191
Percent Similarity: 97.95% Conservative: 0
Best Local Similarity: 97.95% Mismatches: 2
Query Match: 58.03% Indels: 4
DB: 17 Gaps: 0

US-10-030-937-9 (1-193) x US-10-170-385-390 (1-2478)

QY 1 MetGlnSerLeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrPro 20
|||||
Db 96 ATGAGTCCCTGATGAGGCTCCCTCTGTATCGCCCTGGGCTTGCTTCTCGGACCCCT 155
QY 21 AlaGlnAlaHisLeuLysLysProSerGlnLeuSerSerPheSerTrpAspAsnCysPhe 40
|||||
Db 156 GCGCAAGCCACCTGAAAGCCATCCAGCTCAGTAGCTTTTCTGGGATAACTGTGA- 214
QY 41 -GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVa 60
|||||
Db 215 TGAAGGGAAGGACCCCTGCGGTGATCAGAAGCCCTGACTCTGGAGCCCTGACCCCATCGTCT 274
QY 60 lProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLe 80
|||||
Db 275 TCCTGGAATGTGACCTCAGTGTCTGGGAGGAGGAGTGTCCCTGAGTTCTCCTCT 334
QY 80 uLysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCysTh 100
|||||
Db 335 GAAGGTGGATTAGTTTGGAGAAGGAGGTGGCTCTGGATCAAGATCCCATGCAC 394
QY 100 rAspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIlePr 120
|||||
Db 395 AGACTACATTGGCAGCTGTACCTTTGAACACTTCTGTGATGTGCTTGACATGTTAATTC 454
QY 120 oThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPh 140
|||||
Db 455 TACTGGGAGCCCTGCCAGAGCCCTGCGTACCTATGGGCTTCTTGGCCTGACCTGTCCTT 514
QY 140 eLysGluGlyThrTyrSerLeuProLysSerGluPheAla-ValProAspLeuGluLeuP 160
|||||
Db 515 CAAAGAAGGAACCTACTCACTGCCCAAGAGCGAATTCTGT-TGTGCTGACCTGGAGCTGC 573
QY 160 roSerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysA 180
|||||
Db 574 CCAGTTGGCTCACCAACCGGAACCTACCGCATAGAGAGCGTCTTGAGCAGCAGTGGGAAGC 633
QY 180 rgLeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle 193
|||||
Db 634 GTCTGGCTGCATCAAGATCGCTGCCTCTCTAAAGGGCATA 674

RESULT 8
US-10-723-860-5187
; Sequence 5187, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5187
; LENGTH: 3988
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2864)..(2894)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3472)..(3486)
; OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-5187

Alignment Scores:
Pred. No.: 5.92e-102 Length: 3988
Score: 112.00 Matches: 152
Percent Similarity: 98.70% Conservative: 0
Best Local Similarity: 98.70% Mismatches: 1
Query Match: 58.03% Indels: 2
DB: 20 Gaps: 0

US-10-030-937-9 (1-193) x US-10-723-860-5187 (1-3988)

QY 41 GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVal 60
|||||
Db 216 GAAGGGAAGGACCCCTGCGGTGATCAGAAGCCCTGACTCTGGAGCTGACCCCATCGTCTG 275
QY 61 ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLeu 80
|||||
Db 276 CTTGGAATGTGACCTCAGTGTCTGGGAGGAGTGTCCCTGAGTTCTCCTCTG 335
QY 81 LysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCysThr 100
|||||
Db 336 AAGGTGGATTAGTTTGGAGAAGGAGGTGGCTCTGGATCAAGATCCCATGCACA 395
QY 101 AspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIlePro 120
|||||
Db 396 GACTACATTGGCAGCTGTACCTTTGAACACTTCTGTGATGTGCTTGACATGTTAATTCCT 455
QY 121 ThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProphe 140
|||||
Db 456 ACTGGGAGCCCTGCCAGAGCCCTGCGTACCTATGGGCTTCTTGGCCTGACCTGTCCCTTC 515
QY 141 LysGluGlyThrTyrSerLeuProLysSerGluPheAla-ValProAspLeuGluLeuPr 160
|||||
Db 516 AAAGAAGGAACCTACTCACTGCCCAAGAGCGAATTCTGT-TGTGCTGACCTGGAGCTGCC 574
QY 160 oSerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysAr 180
|||||
Db 575 CAGTTGGCTCACCAACCGGAACCTACCGCATAGAGAGCGTCTTGAGCAGCAGTGGGAAGCG 634
QY 180 gLeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle 193
|||||
Db 635 TCTGGCTGCATCAAGATCGCTGCCTCTCTAAAGGGCATA 674


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RESULT 9
US-09-864-761-1518/c
; Sequence 1518, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 1518
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011342.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.99
US-09-864-761-1518

Alignment Scores:
Pred. No.: 1.69e-51 Length: 475
Score: 61.00 Matches: 61
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 31.61% Indels: 0
DB: 9 Gaps: 0

US-10-030-937-9 (1-193) x US-09-864-761-1518 (1-475)

Qy 82 ValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCysThrAsp 101
Db 465 GIGGATTTAGTTTGGAGAGAGAGGTGGCTCTGGATCAAGATCCCATGCACAGAC 406
Qy 102 TyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIleProThr 121
Db 405 TACATTGGCAGCTGTACCTTTGAACACTTCTGTGATGTGCTTGACATGTTAATTCCTACT 346
Qy 122 GlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPheLys 141
Db 345 GGGAGGCCCTGCCAGAGCCCCCTGCGTACCTATGGGCTTCCTTGCCACTGTCCTTCAAA 286
Qy 142 Glu 142
Db 285 GAA 283

RESULT 10
US-09-864-761-18277/c
; Sequence 18277, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
```


.; LOCATION: (55290)..(55389)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (56674)..(56773)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (57879)..(57978)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (78952)..(79051)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (85316)..(85415)
; OTHER INFORMATION: n is a, c, g, or t
US-10-225-810-26

Alignment Scores:
Pred. No.: 6.32e-28 Length: 250000
Score: 40.00 Matches: 40
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.73% Indels: 0
DB: 16 Gaps: 0

US-10-030-937-9 (1-193) x US-10-225-810-26 (1-250000)

QY 154 ValProAspLeuGluLeuProSerTrpLeuThrThrGlyAsnTyArgIleGluSerVal 173
|||||
Db 249596 GTGCCTGACCTGGAGCTGCCAGTTGGCTCACCACCGGAACACTACCGCATAGAGCGTC 249537

QY 174 LeuSerSerSerGlyLysArgLeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle 193
|||||
Db 249536 CTGAGCAGCAGTGGGAAGCGTCTGGCTGCATCAAGATCGCTGCCTCTCTAAAGGGCATA 249477

RESULT 13
US-10-027-632-207798
; Sequence 207798, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 10827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207798
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-207798

Alignment Scores:
Pred. No.: 3.35e-08 Length: 546

Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.33% Indels: 0
DB: 13 Gaps: 0

US-10-030-937-9 (1-193) x US-10-027-632-207798 (1-546)

QY 41 GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProile 58
|||||
Db 297 GAAGGGAAGGACCCCTGGGTGATCAGAAGCCTGACTCTGGAGCCTGACCCCATC 350

RESULT 14

US-10-027-632-207799
; Sequence 207799, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 10827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207799
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-207799

Alignment Scores:
Pred. No.: 3.35e-08 Length: 546
Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.33% Indels: 0
DB: 13 Gaps: 0

US-10-030-937-9 (1-193) x US-10-027-632-207799 (1-546)

QY 41 GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProile 58
|||||
Db 297 GAAGGGAAGGACCCCTGGGTGATCAGAAGCCTGACTCTGGAGCCTGACCCCATC 350

RESULT 15

US-10-027-632-207800
; Sequence 207800, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 10827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676

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; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 207800
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-207800

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Alignment Scores:	
Pred. No.:	3.35e-08
Score:	18.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	9.33%
DB:	13
Length:	546
Matches:	18
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-030-937-9 (1-193) x US-10-027-632-207800 (1-546)

Qy 41 GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIle 58
|||
Db 297 GAAGGGAAGGACCCTGCGGTGATCAGAGCCTGACTCTGGAGCCTGACCCGATC 350

Search completed: July 28, 2005, 02:06:19
Job time : 1211.74 secs

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